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PROVISIONAL APPLICATION FOR PATENT COVER SHEET

This is a request for filing a PROVISIONAL APPLICATION FOR PATENT under 37 CFR 1.53(c).

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INVENTOR(S)		
Given Name (first and middle [if any])	Family Name or Surname	Residence (City and either State or Foreign Country)
Chaker	Adra	Boston, MA

Additional inventors are being named on the _____ *separately numbered sheets attached hereto*

TITLE OF THE INVENTION (500 characters max)

IDENTIFICATION OF GRANULOCYTE SUBTYPE-SELECTIVE RECEPTORS AND ION CHANNELS BY USING A HIGH-DENSITY OLIGONUCLEOTIDE PROBE ARRAY

Direct all correspondence to: **CORRESPONDENCE ADDRESS**

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ENCLOSED APPLICATION PARTS *(check all that apply)*

☒ Specification *Number of Pages* 18 ☐ CD(s), Number _____

☒ Drawing(s) *Number of Sheets* 35 ☒ Other (specify) Attachment 1370

☐ Application Data Sheet. See 37 CFR 1.76

METHOD OF PAYMENT OF FILING FEES FOR THIS PROVISIONAL APPLICATION FOR PATENT

☒ Applicant claims small entity status. See 37 CFR 1.27.

☒ A check or money order is enclosed to cover the filing fees.

☒ The Director is hereby authorized to charge filing fees or credit any overpayment to Deposit Account Number: 50-0850 for deficiencies

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FILING FEE Amount ($): 80.00

The invention was made by an agency of the United States Government or under a contract with an agency of the United States Government.

☐ No.

☒ Yes, the name of the U.S. Government agency and the Government contract number are: NIH Grant AI 43663 from the National Institute of Allergy and Infectious Diseases and by Grant RSG-01-241-01-LIB from the American Cancer Society (to C.A.).

Respectfully submitted,

SIGNATURE _____

TYPED or PRINTED NAME David S. Resnick

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Date March 3, 2004

REGISTRATION NO. 34,235 *(If appropriate)*

Docket Number: 732892-055040-P

The PTO did not receive the following listed item(s) Claims and small entity

USE ONLY FOR FILING A PROVISIONAL APPLICATION FOR PATENT

PTO/SB/17 (10-03)
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FEE TRANSMITTAL for FY 2004

Effective 10/01/2003. Patent fees are subject to annual revision.

[X] Applicant claims small entity status. See 37 CFR 1.27

TOTAL AMOUNT OF PAYMENT ($) 80.00

Complete if Known	
Application Number	To be assigned
Filing Date	Herewith
First Named Inventor	C. Adra
Examiner Name	
Art Unit	
Attorney Docket No.	732892-055040-P

METHOD OF PAYMENT *(check all that apply)*

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FEE CALCULATION

1. BASIC FILING FEE

Large Entity Fee Code	Large Entity Fee ($)	Small Entity Fee Code	Small Entity Fee ($)	Fee Description	Fee Paid
1001	770	2001	385	Utility filing fee	
1002	340	2002	170	Design filing fee	
1003	530	2003	265	Plant filing fee	
1004	770	2004	385	Reissue filing fee	
1005	160	2005	80	Provisional filing fee	80.00

SUBTOTAL (1) ($) 80.00

2. EXTRA CLAIM FEES FOR UTILITY AND REISSUE

		Extra Claims		Fee from below		Fee Paid
Total Claims		-20** =		X	=	
Independent Claims		- 3** =		X	=	
Multiple Dependent					=	

Large Entity Fee Code	Large Entity Fee ($)	Small Entity Fee Code	Small Entity Fee ($)	Fee Description
1202	18	2202	9	Claims in excess of 20
1201	86	2201	43	Independent claims in excess of 3
1203	290	2203	145	Multiple dependent claim, if not paid
1204	86	2204	43	** Reissue independent claims over original patent
1205	18	2205	9	** Reissue claims in excess of 20 and over original patent

SUBTOTAL (2) ($)

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FEE CALCULATION (continued)

3. ADDITIONAL FEES

Large Entity Fee Code	Large Entity Fee ($)	Small Entity Fee Code	Small Entity Fee ($)	Fee Description	Fee Paid
1051	130	2051	65	Surcharge - late filing fee or oath	
1052	50	2052	25	Surcharge - late provisional filing fee or cover sheet	
1053	130	1053	130	Non-English specification	
1812	2,520	1812	2,520	For filing a request for *ex parte* reexamination	
1804	920*	1804	920*	Requesting publication of SIR prior to Examiner action	
1805	1,840*	1805	1,840*	Requesting publication of SIR after Examiner action	
1251	110	2251	55	Extension for reply within first month	
1252	420	2252	210	Extension for reply within second month	
1253	950	2253	475	Extension for reply within third month	
1254	1,480	2254	740	Extension for reply within fourth month	
1255	2,010	2255	1,005	Extension for reply within fifth month	
1401	330	2401	165	Notice of Appeal	
1402	330	2402	165	Filing brief in support of an appeal	
1403	290	2403	145	Request for oral hearing	
1451	1,510	1451	1,510	Petition to institute a public use proceeding	
1452	110	2452	55	Petition to revive - unavoidable	
1453	1,330	2453	665	Petition to revive - unintentional	
1501	1,330	2501	665	Utility issue fee (or reissue)	
1502	480	2502	240	Design issue fee	
1503	640	2503	320	Plant issue fee	
1460	130	1460	130	Petitions to the Commissioner	
1807	50	1807	50	Processing fee under 37 CFR 1.17(q)	
1806	180	1806	180	Submission of Information Disclosure Stmt	
8021	40	8021	40	Recording each patent assignment per property (times number of properties)	
1809	770	2809	385	Filing a submission after final rejection (37 CFR 1.129(a))	
1810	770	2810	385	For each additional invention to be examined (37 CFR 1.129(b))	
1801	770	2801	385	Request for Continued Examination (RCE)	
1802	900	1802	900	Request for expedited examination of a design application	

Other fee (specify) _____

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SUBMITTED BY				(Complete *if applicable*)	
Name *(Print/Type)*	David S. Resnick	Registration No. *(Attorney/Agent)*	34,235	Telephone	(617) 345-6057
Signature				Date	3/3/04

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Practitioner's Docket No. 732892-055040-P *PATENT*

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:	Chaker Adra		
Application No.:	To be assigned	Group No.:	To be assigned
Filed:	Herewith	Examiner:	To be assigned
For:	IDENTIFICATION OF GRANULOCYTE SUBTYPE-SELECTIVE RECEPTORS AND ION CHANNELS BY USING A HIGH-DENSITY OLIGONUCLEOTIDE PROBE ARRAY		

MAIL STOP PROVISIONAL APPLICATION
Commissioner for Patents
P.O. Box 1450
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EXPRESS MAIL CERTIFICATE

"Express Mail" Label Number: EU 813933419 US
Date of Deposit: March 3, 2004

I hereby state that the following *attached* papers and fees:

1. Provisional Application for Patent Cover Sheet (1 pp.);
2. Provisional Patent Application (1423 pp.): Specification – 18 pp.; Drawings – 35 sheets; Attachment – 1370 pp.;
3. Fee Transmittal (1 pg.);
4. Check in the Amount of $ 80.00;
5. Return Receipt Postcard;

are being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 C.F.R. section 1.10, on the date indicated above and is addressed to Box Provisional Application, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

Nicole M. Gignac

Nicole M. Gignac
Signature of person mailing paper or fee

IDENTIFICATION OF GRANULOCYTE SUBTYPE-SELECTIVE RECEPTORS AND ION CHANNELS BY USING A HIGH-DENSITY OLIGONUCLEOTIDE PROBE ARRAY

[0001] This invention was made in part with U.S. Government support under NIH Grant AI 43663 from the National Institute of Allergy and Infectious Diseases and by Grant RSG-01-241-01-LIB from the American Cancer Society (to C.A.). The U.S. Government has certain rights in this application.

FIELD OF THE INVENTION

[0002] The present invention relates to the identification of granulocyte subtype-selective receptors and ion channels that can be use as targets for drug discovery.

BACKGROUND OF THE INVENTION

[0003] Three types of human blood granulocytes, eosinophils, basophils and neutrophils, play roles in protecting against microbial infection by releasing cell type-specific mediators and proteases. Specifically, eosinophils and basophils evoke allergic reactions as well as damage nematodes. [1,2] As well as killing bacteria, neutrophils sometimes induce systemic vasculitis or multiple organ damage under certain conditions. [3,4] Thus, targeting granulocyte type-selective functions is considered an important strategy for drug discovery.

[0004] Activation of blood granulocytes and tissue mast cells is generally characterized by an influx of extracellular calcium (Ca^{2+}), which is essential for subsequent release of granule-derived mediators, newly generated lipid mediators and cytokines. [5] The mechanism by which granulocyte mediator secretion is sustained is therefore likely to include modulation of various types of ion channels. Flow of ions including K^+ and Cl^- may play an important role during granulocyte responses because they regulate cell membrane potential and thus influence Ca^{2+} influx. [6] Treatment of mast cells and basophils with pertussis toxin inactivates the Gi-type of G-proteins and abolishes degranulation induced by non-immunological ligands such as thrombin and N-formylpeptide; however, it fails to inhibit the influx of Ca^{2+}. [7] Thus, Ca^{2+}-independent

stimulation of Gi is also involved in granulocyte degranulation. The thrombin (protease) activated receptors and formylpeptide receptors are classified as G protein-coupled receptors (GPR), having an extracellular N-terminal segment, a seven transmembrane region, which forms the transmembrane core; three exoloops, three cytoloops, and a C-terminal segment. [8] Thus, ion channels and GPR both play essential roles in degranulation as well as other cellular function important for granulocytes. As a result, both ion channels and GPR are targets of drug development. [9]

[0005] As the human genome project nears completion, the identification of potential drug targets using gene expression profiles from specific cell types is becoming practical and important for drug discovery. [10,11] The sequencing of the human genome is offering an unprecedented opportunity for the pharmaceutical development of drugs. Receptor genes and ion channel genes are found only in 5% and 1.3% of all genes present in the human genome, [10] respectively. However, receptors and ion channels are respectively found in 45% and 5% of the molecular targets of all known drugs. [9,12,13] Thus, receptors including GPR and ion channels are now considered as the most important drug targets.

[0006] Until recently, it has been impractical to analyze genome-wide expression of leukocytes. Newly developed technology, the microarray or high density oligonucleotide probe array (GeneChip) is one of the latest breakthroughs in experimental molecular biology, which allows approximately 39,000 transcripts derived from a cells transcriptome to be simultaneously monitored. Using this technology, we previously reported the transcriptome profiling of various types of mast cells and eosinophils. [14-16] However, there is still a need in the art to identify drug targets that are selectively, or preferentially, expressed in specific cell types such that efforts required for pharmaceutical development are minimized.

SUMMARY OF THE INVENTION

[0007] In the present study, we used GeneChip (version U133A containing approximately 22,000 gene probes) to examine the cell type-selective transcriptome expression of 7 types of leukocytes (basophils, eosinophils, neutrophils, $CD4^+$ cells, $CD8^+$ cells, $CD14^+$ cells and $CD19^+$ cells), platelets, mast cells and fibroblasts by focusing on the expression of granulocyte-selective genes for ion channels, GPR and other receptors. We identified many novel granulocyte subtype-selective transcripts that are useful for drug development.

[0008] Granulocyte subtype selective transcripts were chosen based on several conditions such as the transcript having 5-fold or greater expression level compared to the maximum level of other leukocytes. Fifty-one transcripts were chosen to be preferentially expressed by each granulocyte subtype. Seventeen out of the 51 transcripts have not been previously reported as granulocyte subtype-selective. Among the 17 receptors and ion channels, six were basophil- and/or eosinophil-selective and were not highly expressed by other organs, indicating that they may be potential targets for anti-allergic drugs.

[0009] Utilization of this database (Attachment A) of potential cell type-selective drug targets will minimize the efforts required for pharmaceutical development of drugs for treatment of diseases of the immune system, cancer, cardiac diseases, as well as other diseases.

BRIEF DESCRIPTION OF THE DRAWINGS

[00010] Figure 1 shows Real-time quantitative PCR analysis of granulocyte-selective gene expression. The relative mRNA expression level by each cell type against PBMNC was shown after normalization of mRNA levels for *A.* HTm4 (0.42 per 100 GAPDH), *B.* Ca^{2+} receptor alpha 1D subunit (0.003), *C.* prostaglandin E receptor type 3a2 (0.12), *D.* EMR-1 (0.62), and *E.* aquaporin 9 (0.92) expressed by PBMNC. Ne; neutrophils (n=3), Eo; eosinophils (n=2), Ba, basophils (n=3), CD4; CD4+ cells (n=3), P; PBMNC (n=1).

[00011] Figure 2 shows the demonstration of HTm4 protein on human basophils. Cells on the glass slide were incubated with 2 μg/ml polyclonal rabbit anti-hHTm4 antibody or 2 μg/ml rabbit IgG (H+L) as a control followed by incubation with a secondary antibody, highly cross-adsorbed Alexa Fluor® 546 conjugated goat anti-rabbit IgG (H+L) (Red). After mounting using the Prolong AntiFade Kit, slides were scanned by Zeiss Laser Scanning Microscope 5 Pascal.

[00012] Figures 3A through 3E shows granulocyte subtype-specific transcripts for ion channels and receptors.

[00013] Figures 4A through 4F show a table of "normalized AD" expression levels of various genes in indicated cells and shows corresponding graphs; x axis represents "normalized AD" expression levels.

[00014] Figures 5A through 5D show a table of "normalized AD" levels of various genes in indicated cells and shows corresponding graphs; x axis represents "normalized AD" expression levels.

[00015] Figures 6A through Figure 6R show the complete list of granulocyte subtype-selective transcripts.

DETAILED DESCRIPTION OF THE INVENTION

[00016] In this study, we have used high density oligonucleotide probe array (GeneChip) to measure the expression levels of approximately 20,000 different transcripts in highly purified cells. These cells were basophils, eosinophils, neutrophils, monocytes ($CD14^+$), T lymphocytes ($CD4^+$ and $CD8^+$ cells), B lymphocytes ($CD19^+$), lung-derived mast cells, cord blood-derived cultured mast cells, and nasal polyp-derived fibroblasts. The GeneChip assay allows the simultaneous measurement of large numbers of transcripts using relatively small numbers of cells. Using this technology, we could even measure triplicate transcriptome levels of basophils, the most rare granulocytes in peripheral blood.

[00017] Cell type-selective transcripts were selected based on the following criteria; (1) the average "normalized AD" expression level of each gene in a certain cell type must be 3-fold or greater than the maximal level in other cell types, and (2) must be significantly ($p < 0.01$) greater than that in other cell types. (3) The "AD" expression level provided with "absence" or "marginal" call by GeneChip Suite Software should be observed only once or not at all in the three or four independent experiments (3 experiments for basophils, 4 experiments for eisinophils and neutrophils) using different cell populations performed. (4) For the transcripts preferentially expressed for the two different cell types such as basophils and eosinophils, the average "normalized AD" expression levels in the two cell types should be within 3-fold of each other. Using these standards, we found 83 basophil-selective, 37 eosinophil-selective, 257 neutrophil-selective, 34 basophil-eosinophil-selective, 19 eosinophil-neutrophil-selective, and 17 basophil-neutrophil-selective transcripts. Due to the functional similarity with basophils, mast cell-selective transcripts were also examined, and 63 mast cell-selective and 11 mast cell-basophil-selective transcripts were also detected (Table 1, and Figures 6A-6R). Since mast cells, basophils and eosinophils play similar roles in allergic inflammation, the transcripts preferentially expressed for the three granulocytes by comparing their average "normalized AD"

levels to other leukocytes. Thirty-four transcripts were then selected; however, most of them were overlapped with the transcripts listed in Figures 6A-6R. Only four transcripts (*MYB*, *SAMSN1*, *BACE2*, and *CASP3*) were found not overlapped, and they were not receptors or ion channels.

[00018] Among the 491 granulocyte-selective transcripts listed in Figures 6A-6R, 4 ion channels, 19 GPR and 28 other receptors were further selected (Figure 3). When plural transcripts obtained by different probe sets had identical Genebank or Unigene accession numbers (http://www.ncbi.nlm.nih.gov/), the transcript showing the highest expression level was selected.

Ion channels and receptors preferentially expressed by granulocytes other than neutrophils

[00019] Eosinophils, basophils and mast cells play an important role in the pathogenesis of allergic diseases, but do not play an essential role in killing microbes except for nematodes. On the other hand, neutrophils play a crucial role in killing microbes such as bacteria. Caution should be taken in regulating neutrophil function even in the case of neutrophil-induced inflammation. Therefore, the molecules present only in granulocytes except for neutrophils would be important pharmaceutical targets for allergic disorders. [1,2]

[00020] Among the 51 granulocyte-selective transcripts for ion channels and receptors, we identified 17 granulocyte-selective transcripts that have not been reported for their selective expression (shown in bold letters in Figure 3). Of these 17 transcripts, eight were preferentially expressed by granulocytes other than neutrophils. Among these eight transcripts, the two transcripts for fibroblast growth factor receptor 2 and low density lipoprotein receptor were found to be expressed by multiple tissue cell types (shown at the Web site http://www.lsbm.org/index_e.html), which displays genomic expression of 55 different human tissue cells such as brain, heart and lung cells using the same experimental system. Affymetrix, U133A as ourts. Thus, they may not be suitable as a drug target because important organs that are unrelated to allergic inflammation (such as the brain) express it. Among the six novel transcripts found to be preferentially expressed by granulocytes except for neutrophils, we focus on the following four transcripts expressed by granulocytes including basophils. They were Ca^{2+} channel (*CACNA1D*), a prostaglandin E receptor, (*EP3A2)*, epidermal growth factor-like module-containing mucin-like receptor (EMR) 1 (*EMR1*), and HTm4 (*MS4A3*).

[00021] Basophils are the rarest granulocytes present in human peripheral blood and as such their complete transcriptional profiles remain unclear and no basophil-selective transcripts have previously been reported. [21] Although eosinophils and mast cells have been considered as important therapeutic targets for allergic diseases for a long time, recent studies suggest the importance of basophils in pathogenesis of severe allergic diseases such as fatal asthma. [2,22] Therefore, we further examined the selective expression of these four basophil-, or basophil-eosinophil-selective transcripts by using real-time RT-PCR. As shown in the Fig. 1, including a known molecule preferentially expressed by neutrophils, aquaporin 9, [23] the results obtained with GeneChip assay were confirmed by using this highly accurate and reproducible method. [24]

[00022] Among these four molecules, we could obtain a suitable antibody against HTm4, which is a member of a family of four transmembrane- proteins which include CD 20 and high affinity Fc receptor for IgE (FcεRI) β-chain. [25] Genetics provided evidence for the existence of multiple loci relevant to atopic asthma on chromosome 11q13, including HTm4. [26] Most recently, we have published data identifying HTm4 as a hematopoietic cell cycle regulator. [27] Using specific antibody against HTm4, we could detect the expression of HTm4 at the protein level in basophils (Fig. 2). To confirm whether these ion channels and receptors could be potential drug targets for diseases involving basophil activation, the amount of molecules expressed by various cell types should be quantified and the effect of any identified antagonists should be tested on the cell types found to express these molecules.

[00023] As has been well documented and expected, Fc ε RI α, IL-3 receptors, IL-5 receptors, chemokine receptor CCR3, [1,2] sialic acid binding Ig-like lectin (Siglec)-8, [28] Siglec-6, [15] histamine H4 receptor [29] and chemoattractant receptor- homologous molecule expressed on Th2 cells (CRTH2) [30] were preferentially expressed by basophils and/or eosinophils or mast cells. These consistent observations strengthened the reliability of the present methods and research strategy. Indeed, the antibody against Siglec-8 can induce selective apoptosis of eosinophils, and is expected to be useful therapeutically. [28]

Ion channels and receptors preferentially expressed by granulocytes including neutrophils

[00024] Of the 17 transcripts that have not been reported as granulocyte-selective, nine were preferentially expressed by granulocytes including neutrophils. Pharmaceutical targets

of selective granulocyte transcripts should treat inflammatory diseases without affecting the function of important organs that are unrelated to inflammation as well as the function of lymphocytes. However, four of the nine neutrophil-selective transcripts were expressed by multiple organ tissues. One of the four neutrophil-selective transcripts encoded proteinase-activated receptor (PAR)-2, a receptor for mast cell tryptase, which is linked to the pathogenesis of allergic diseases such as asthma. [31,32] PAR-2 transcripts are also abundantly expressed by tissue types including skin and intestine which are often the target organs for allergic diseases. But the development of PAR-2 antagonists for use as anti-allergic drugs may be unsuitable because it may down regulate neutrophil function and thereby induce bacterial infection.

General discussion

[00025] We identified 51 granulocyte-selective genes for ion channels and receptors by examining approximately 20,000 kinds of transcripts derived from 16,000 genes from 10 different types of cells using U133A GeneChip, which covers approximately half of the genes present in the human genome. The majority of these transcripts encoded molecules known or expected to be granulocyte subtype-selective such as the IL-3 receptor and Fc ε receptors.

[00026] Mast cells expressed low levels of Fc ε RI α compared to basophils, and that even neutrophils expressed a substantial level of the receptor (Figure 3). This raises the possibility that GeneChip assay may not be suitable for detecting selective molecules. In the present study, however, only the GeneChip data obtained using cord blood-derived mast cells and lung mast cells could be employed due to the strict data selection based on the RNA quality (see Methods). As has bee reported,[14, 33] peripheral blood-derived cultured mast cells or skin-derived mast cells expressed approximately 10-fold Fc ε RI α mRNA compared to cord blood-derived mast cells (data not shown). Also, as shown in Figures 6A-6R, only 2 of the 4 neutrophil samples expressed Fc ε RI α mRNA. This may be explained by the observation that only neutrophils obtained from some allergic donors express the molecule.[34]

[00027] We unexpectedly found 17 granulocyte-selective transcripts including HTm4. Basophil- and/or eosinophil-selective transcripts identified in our study could be potential therapeutic targets for allergic diseases because these granulocytes play a crucial role in allergic inflammation. [1,2] Granulocyte-selective transcripts could also be drug targets for other inflammatory diseases such as systemic vasculitis. [3,4] Analysis of cell type-selective transcripts

from database searches is expected to minimize the efforts required for drug discovery. The public database (http://www.lsbm.org/index_e.html) shows that some granulocyte-selective transcripts (18 out of 51) detected in our study are abundantly expressed by multiple (more than 3) organ tissue cell types using the same GeneChip U133A probe array. Thus, the safety of any candidate drug must be evaluated by comparing its efficacy (on granulocytes) with its toxicity (to organs). Six out of the 17 novel granulocyte-selective molecules may be excluded from drug development due to their expression in multiple organs unrelated to the diseases. Thus, our approach has identified 11 receptors and ion channels with therapeutic potential. Especially, among the 11 receptors and ion channels, seven were basophil- and/or eosinophil-selective and were not expressed by other organs, indicating that they may be potential targets for anti-allergic drugs.

[00028] Finally, it should be stressed that basophils, the rarest leukocytes, have recently been found to play a more crucial role than we ever proposed in the pathogenesis of intractable allergic diseases such as fatal asthma.[35, 36] Thus, targeting basophil receptors and ion channels such as HTm4 and Ca^{2+} channel CACNA1D is particularly expected for the future drug discovery. The importance of molecules known to be expressed by basophils may be reevaluated regarding its selectivity. Freshly-isolated resting basophils expressed the highest level of IL-4 compared to other cell types. Because the basophil purification procedure requires more isolation steps, ex vivo manipulation may activate the cells. However, it should also be noted that basophils have been recently found as the major source of IL-4 at least in asthma models.[37, 38]

Materials and Methods

Purification of leukocytes

[00029] All human subjects in this study provided written, informed consent, and the Ethical Review Boards at the relevant hospitals (National Center for Child Health and Development, and Jikei University School of Medicine) approved the study. The subjects used in this study were all healthy volunteers, especially having no allergic diseases.

[00030] Granulocytes and mononuclear cells were separated from venous blood of normal volunteers. Human basophils were semipurified by means of Percoll (Pharmacia, Uppsala, Sweden) density gradient centrifugation, and the cells were further purified by negative selection through use of a MACS Basophil Isolation Kit (Miltenyi BioTech, Bergisch-Gladbach,

Germany), as described previously. [17] Eosinophils were isolated by using Percoll (1.090 g/mL) density centrifugation. The eosinophils were further purified by negative selection with anti-CD16-bound micromagnetic beads, as described previously. [18] Neutrophils were isolated by using Percoll (1.085 g/mL) density centrifugation and further purified by negative selection using anti-CD81 antibody and antimouse IgG-bound micromagnetic beads to eliminate contaminating eosinophils. These granulocytes purified from human peripheral blood were spun down onto slide glass by Cytospin II (Shandon Southern Instruments, Inc., Sewickley, PA). The purity of these cells was evaluated based on 500 cells stained with May-Grünwald and Giemsa solutions.

[00031] For preparation of lymphocytes and monocytes, peripheral blood mononuclear cells (PBMNC) were isolated by centrifugation on lymphocyte separation medium (Organon Teknika Corp., Durham, NC). Monocytes ($CD14^+$ cells) were prepared using magnetic beads-conjugated $CD14^+$ antibody (CD14 MicroBeads; Miltenyi Biotec) from PBMNC. $CD4^+$ and $CD8^+$ cells were also respectively sorted using magnetic beads-conjugated $CD4^+$ (CD4 MicroBeads; Miltenyi Biotec) and $CD8^+$ antibodies (CD8 MicroBeads; Miltenyi Biotec) from PBMNC after depletion of $CD14^+$ cells with MACS CD14 MicroBeads (Miltenyi Biotec). The purity of $CD4^+$, $CD8^+$ and $CD14^+$ cells was evaluated by staining the magnetic beads- conjugated cells compared to feasible control cell preparations such as unpurified cells with FITC-labeled goat anti-mouse Immunoglobulin (BD Pharmingen, Tokyo, Japan). Peripheral B cells were purified by a combination of negative (MicroBeads-conjugated antibodies to CD3, CD7, CD14, CD42b, and CD56; Miltenyi Biotec) and positive (CD19 MicroBeads; Miltenyi Biotec) selection using MicroBeads (Miltenyi Biotec). To obtain platelet rich plasma, blood samples were mixed with 3.8% (w/v) sodium citrate solution (9:1) and centrifuged at 260x g for 15 min. at 20°C. To remove any contaminating erythrocytes and leukocytes, the plasma was centrifuged again at 260x g for 15 min.

[00032] Human mast cells were derived from cord blood $CD34^+$ progenitor cells as described previously. [11-14] Briefly, progenitor cells purified from peripheral blood by $CD34^+$ isolation kits (Miltenyi Biotec), were cultured in Iscove's modified Dulbecco medium supplemented with 1% insulin-transferrin-selenium supplements (Life Technologies), 50 μM 2-mercaptoethanol, antibiotics, and 2% fetal calf serum in the presence of 100 ng/ml stem cell

factor and 50 ng/ml IL-6. After 11 to 14 weeks of culture, tryptase positive cells represented more than 99% of the cells.

Purification of human lung mast cells and nasal polyp-derived fibroblasts

[00033] Normal human lung tissue dissected during surgery was obtained macroscopically after informed consent. Human lung mast cells were dispersed from chopped lung specimens by an enzymatic procedure and were purified by magnetic bead affinity selection using the mAb anti-kit, YB5.B8 (BD PharMingen, San Diego, CA) as described previously. [19] The cells were further cultured in the presence of SCF and interleukin 6 (IL-6) for several weeks. Human nasal polyp-derived fibroblasts were obtained as previously reported. [20]

GeneChip expression analysis

[00034] Human genome-wide gene expression was examined using the Human Genome U133A probe array (GeneChip, Affymetrix, Santa Clara, CA), which contains the oligonucleotide probe set for 22,000 full-length genes. Experiments were performed in accordance with the manufacturer's protocol (Expression Analysis Technical Manual) and previous reports. [11-14] Total RNA (3–10 μg) was extracted from 10^7 cells. Double-stranded cDNA was synthesized using a SuperScript Choice system (Life Technologies) and a T7-(dT)24 primer (Amersham Pharmacia Biotech, Buckinghamshire, UK). The cDNA was subjected to *in vitro* transcription in the presence of biotinylated nucleoside triphosphates using a BioArray high-yield RNA transcript labeling kit (Enzo Diagnostics, Farmingdale, NY). The biotinylated cRNA was hybridized with a probe array for 16 h at 45°C. In some experiments as indicated in the supplementary table, biotinylated cRNA was prepared using two-cycles of cDNA synthesis and *in vitro* transcription for target amplification was performed according to the manufacturer's "The Small Sample Labeling Protocol version II" (Affymetrix, Inc). For the latter protocol, we employed 100 ng total RNA. After washing, the hybridized, biotinylated cRNA was stained with streptavidin-phycoerythrin (Molecular Probes, Eugene, OR) and then scanned with a HP gene array scanner. The fluorescence intensity of each probe was quantified using a computer program, GeneChip Analysis Suite 5.0 (Affymetrix). The expression level of single mRNA was determined as the average fluorescence intensity among the intensities obtained by 11 paired (perfect- matched and single nucleotide-mismatched) probes. If the intensities of mismatched

probes were very high, gene expression was judged to be absent, even if a high average fluorescence was obtained with the GeneChip Analysis Suite 5.0 program. The level of gene expression was determined as the average difference (AD) using the GeneChip software. Each AD level was then normalized by dividing it with the median value of 22,283 AD levels obtained in an experiment ("normalized AD" level).

Real-time reverse transcriptase (RT)-PCR

[00035] Total RNA was isolated using Isogen (Nippon gene, Tokyo, Japan) according to the manufacturer's instructions and quantified by measuring the absorbance at 260 nm. RNA was subsequently treated with DNase I (Life Technologies) reverse transcribed using Superscript II reverse transcriptase (Life Technologies). Real-time RT-PCR was performed 10 ng cDNA in 25 µl of final volume using the primers and probes supplied by "Assays-on-Demand Gene Expression system" (PE Applied Biosystem) according to the manufacturer's instructions. Measurement of gene expression was performed using the ABI PRISM 7700 Sequence Detector. The expression level of each gene was normalized to a GAPDH.

Staining of basophils with anti-HTm4

[00036] Basophils purified from human peripheral blood with Basophil Isolation Kit (Miltenyi Biotec) were spun down onto slide glass by Cytospin II (Shandon Southern Instruments Inc., Sewickley, PA). Cells were fixed with aceton for 1 minute and then blocked in goat serum in 50 mm TRS-Cl, pH 7.4 for 1 hour. Cells were further incubated for 2 hours with 2 µg/ml of the polyclonal antibody rabbit anti-hHTm4. Cells were then washed three times with PBS and incubated with a secondary antibody, highly cross-adsorbed Alexa Fluor® 546-conjugated goat anti-rabbit IgG (H+L) (Red) (Molecular Probes, Eugene, OR) for one hour. After three PBS washes, air dried cells were further mounted using the Prolong Anti-Fade Kit (Molecular Probes, Eugene, OR). Slides were scanned by Zeiss Laser Scanning Microscope 5 Pascal (Carl Zeiss Microimaging Inc, Thornwood, NY).

Purity and viability of the leukocytes, and RNA quality

[00037] We used leukocyte samples in this study only if the purity of each cell type was at least 98%, but there are >0.5% contaminated cells in any of the samples. We could

not evaluate the purity of $CD19^+$ cells and platelets due to lack of feasible controls or methods. However, specific transcript markers for non-granulocytes (CD4, CD8, CD14, CD19, IgG, etc.) as well as granulocyte subtype-specific transcripts were reasonably expressed by each leukocyte type as shown in Figures 6A-6R. Regarding the viability, we qualified the RNA before GeneChip assay using Array Quality Metrics Comparisons Software (Affymetrix) as well as trypan blue staining (they were always >95% viable), since RNAse-rich granules derived from degenerating cells rapidly destroy RNA transcripts. Briefly, to evaluate the quality of RNA, the ratio of 3'-probe set and 5'-probe set of housekeeping genes were compared as shown in Figures 6A-6R. According to the above software's guidance, the ratio of >2:1 at standard sample (5μg total RNA) protocol and that of >10:1 at small sample (50 ng total RNA) protocol were recommended. As shown in Figures 6A-6R, the cells used in the present study had the appropriate ratios of 3'-probe set and 5'-probe set of housekeeping genes, suggesting that these cells were highly viable.

Statistical analysis

[00038] Since logarithmic "normalized AD" levels were normally distributed within each group, unpaired parametric Student's two-tailed *t*-test was employed to analyze the data on a logarithmic scale.

Table 1. Representative cell type-selective transcripts in granulocytes

Accession # [a]	Transcript	S.I. [b]	Normalized AD level
	Basophil-selective		
NM_000589.1	IL-4	73.3	13.3
L35848.1	HTm4	38.2	132.1
BC005912.1	Fc ε RI α	12.7	218.9
	Eosinophil-selective		
NM_001140.1	Arachidonate 15-lipoxygenase	74.1	18.3
NM_024703.1	FLJ22593	19.1	29.1
NM_014442.1	Siglec-8	9.8	16.9
	Neutrophil-selective		
NM_004633.1	IL-1 R, type II	127.9	51.5
U73191.1	inward rectifier K^+ channel Kir1.3	107.5	98
NM_001557.1	CXCR2 (IL-8 receptor β)	39.3	105.2
	Mast cell-selective		
AF206667.1	tryptase β	84.3	159.4
NM_001911.1	cathepsin G	51.5	72.1
BC005929.1	major basic protein	31.6	72.5
	Basophil-eosinophil-selective		
M75914.1	IL-5R α	42.8	19.4(B), 29.3(E)
NM_004778.1	CRTH2	16.6	23.9(B), 38.1(E)
NM_001828.3	Charcot-Leyden crystal protein	15.2	229.2(B), 198.6(E)
	Eosinophil-neutrophil-selective		
NM_005306.1	GPR 43 (PAR1-like)	21.7	11.7(E), 32.9(N)
NM_004668.1	DHHC domain containing 18	6.6	16.2(E), 44.5(N)
	Basophil-neutrophil-selective		
NM_016006.1	CGI-58 protein	5.8	12.6(B), 21.2(N)
	Basophil-mast cell-selective		
NM_001870.1	carboxypeptidase A3	59.2	111.7(M), 137.3(B)
NM_002529.2	TRK neurotrophin receptor	34.7	3.1(M), 7 (B)
NM_000139.1	Fc ε RI β	21.2	22.2(M), 43.8(B)

a. The GenBank accession number (http://www.ncbi.nlm.nih.gov).
b. Selectivity index (S.I.) was calculated by comparing the "normalized AD" level in a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types. The complete list of the genes having >3 S.I. is shown in Supplementary Table 1.

[00039] Figures 6A-6R show the complete list of granulocyte subtype-selective transcripts. Selectivity index (S.I.) was calculated by comparing the "normalized AD" level of a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types including platelets (Pl), $CD4^+$ cells (CD4), $CD8^+$ cells (CD8), $CD14^+$ cells (CD14), CD19+ cells (CD19) and nasal polyp-derived cultured fibroblasts (Fb). Transcripts having S.I. >3-fold were shown in Figures 6A-6R A-H. *A.* Basophil (Ba)-selective transcripts. *B.* Eosinophil (Eo)-selective transcripts. *C.* Neutrophil (Ne)-selective transcripts. *D.* Mast cell (MC)-selective transcripts. *E.* Basophil and eosinophil-selective transcripts. *F.* Eosinophil and neutrophil-selective transcripts. *G.* Basophil and neutrophil-selective transcripts. *H.* Mast cell and basophil-selective transcripts. *I.* Raw AD levels for the median values used to normalize the raw AD levels, and the housekeeping genes. When the result was accompanied by presence call, it was shown as a bold numeral. Italic numerals show that the raw AD levels were associated with absence call by the GeneChip analysis software. 1. Abbreviations used in the tables were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

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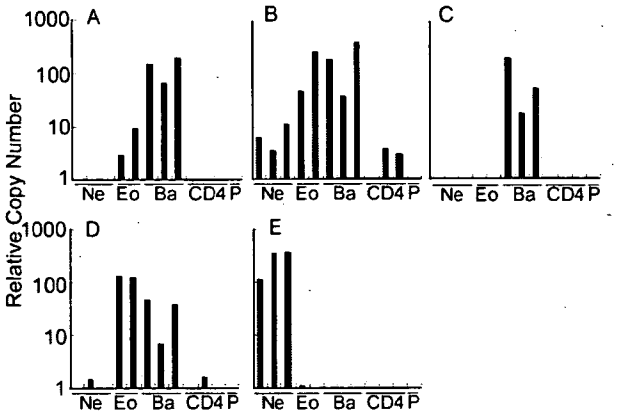
Figure 1



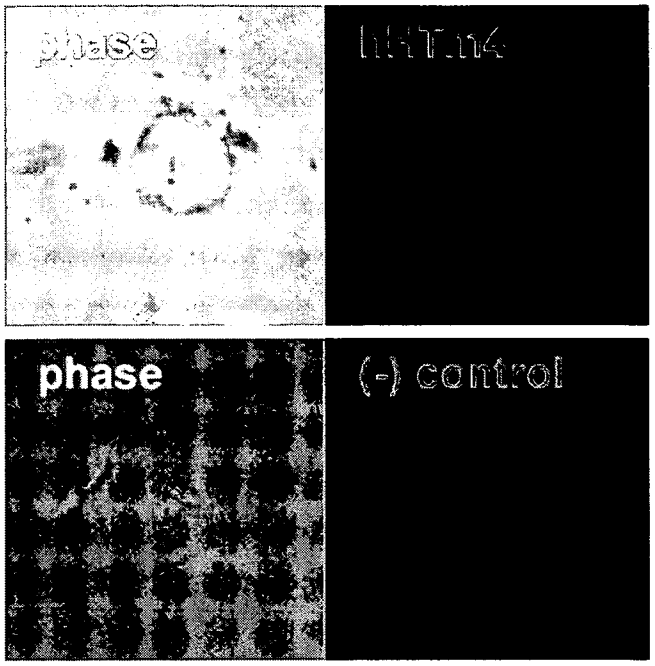


Figure 2

Figure 3A

Figure 3. Granulocyte subtype-specific transcripts for ion channels and receptors

Transcript (Accession #, GenBank)	Cell-type[a]	MC	Ba	Eo	Ne	Pl	CD4	CD8	C D14	CD19	Fb	TC[b]	Gene Functions
Ion Channels													
Ca^{2+} channel type A1 D (BE550599)	Ba, Eo	0.1	1.7	1.5	0.4	0.0	0.3	0.1	0.0	0.3	0.0	*0*	
aquaporin 9 (NM_020980) 602914	Ne	0.7	0.1	0.4	137.4	0.4	0.9	0.1	8.6	0.1	0.2	*7*	facilitates uptake of the metalloids arsenite and antimonite
K^+ channel Kir1.3 (U73191) 600359	Ne	0.9	0.2	0.4	99.5	0.7	0.2	0.0	0.8	0.0	0.0	*5*	Andersen syndrome (170390) and Bartter syndrome (241200)
K^+ channel Kir2.1 (AF153820) 600681	Ne	0.7	3.8	5.3	40.7	0.4	0.2	0.5	1.5	0.7	1.1	*6*	Andersen syndrome (170390) and Bartter syndrome (241200)
GPCR													
histamine H_4 R (AF312230) 606792	Ba	0.7	34.2	9.4	0.7	0.4	0.8	0.5	0.6	0.0	0.1	*0*	expression of HRH4 conferred sensitivity
PGE[c] R type 3a2 (X83858) 176806	Ba	0.8	10.3	0.1	0.7	0.6	0.3	0.2	0.2	0.5	1.7	*0*	signaling pathways
C3a R (U62027) 605246	Ba, Eo	11.8	55.7	39.4	2.0	1.6	1.6	1.5	3.0	0.6	0.5	*3*	anaphylatoxin receptor
CCR3 (NM_001837) 601268	Ba, Eo	0.6	117.4	90.9	24.9	0.2	0.5	0.4	0.2	0.2	0.4	*0*	importance for eosinophil responses
CRTH2 [c](NM_004778) 604837	Ba, Eo	1.1	26.0	38.2	2.0	0.8	1.4	1.0	1.2	0.9	0.5	*0*	mediate signals to the interior of the cell via activation of heterotrimeric G proteins
EMR-1 (NM_001974) 600493	Ba, Eo	0.8	33.5	90.9	4.2	3.4	1.7	0.8	7.1	1.6	0.5	*1*	Probably involved in cellular response to a hormone
adenosine A_3 R (NM_000677) 600445	Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5	*0*	cardioprotective function
P2Y2 purinergic R (NM_002564) 600041	Eo	0.1	0.1	5.5	0.1	0.2	0.1	0.3	1.2	0.2	0.1	*0*	P2RY2 may participate in control of the cell cycle of endometrial carcinoma cells
GPR105 purinergic R (NM_014879)	Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5	*2*	GPR105 is a G-protein-coupled receptor identifying a quiescent, primitive population of hematopoietic cells restricted to bone marrow; GPR105 might play an important role in peripheral and neuroimmune function
GPR, Edg-4 (AF011466) 605110	Eo, Ne	1.3	2.8	15.9	24.2	0.1	3.6	5.0	3.8	1.9	0.9	*2*	edg-4 mrna was expressed in mouse islets; edg-4 (lpa2) r is a distinctive functional marker for ovarian carcinoma, and is expressed both as the wild-type and a carboxyl-terminally extended gain-of-function mutant.
PAR1-like GPR43 (NM_005306)	Eo, Ne	0.3	0.7	12.4	35.2	0.8	0.1	0.1	0.7	0.4	0.1	*0*	the highest levels of gpr43 were

Figure 3B

603823												found in immune cells; gpr43 is highly restricted in hematopoietic tissues
C5a R (NM_001736) **113995**	Ne	2.3	21.6	13.6	92.6	2.3	1.2	0.5	25.6	1.0	0.4	*5*	receptor for the chemotactic and inflammatory peptide anaphylatoxin c5a. this receptor stimulates chemotaxis, granule enzyme release and superoxide anion production.
CXCR1 IL-8R (NM_000634) 146929	Ne	0.2	4.3	0.3	83.4	0.4	0.3	0.2	0.2	0.1	0.1	*0*	receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to mgsa (gro) with a low affinity.
CXCR2 IL-8R (NM_001557)	Ne	0.2	1.1	1.5	112.1	2.7	0.3	0.8	0.7	0.6	0.0	*1*	receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to gro/mgsa and nap-2 also with a high affinity.
formyl peptide R 1 (NM_002029) 136537	Ne	2.8	23.5	8.8	282.9	3.6	1.3	0.7	62.6	1.1	0.5	*0*	HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED

Figure 3C

													VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
formyl peptide R 2 (U81501)	Ne	0.4	0.5	0.6	75.5	0.1	1.0	0.6	6.0	0.8	0.1	*5*	likely FPR2, mediates superoxide production at high concentrations of fMLF
GPR77 (NM_018485)	Ne	0.1	0.9	0.8	3.4	0.0	0.3	0.2	1.0	0.1	0.3	*2*	C5L2 is an anaphylatoxin-binding protein with unique ligand binding and signaling properties
GPR86 purinergic R (NM_023914)	Ne	0.3	0.2	17.9	88.2	1.9	0.1	0.2	12.3	0.6	0.0	*1*	GPR86 proved to be a G(i)-coupled receptor displaying a high affinity for ADP, similar to the P2Y(12) receptor and can therefore be tentatively called P2Y(13)
PAR2 (BE965369) **600933**	Ne	0.1	0.3	2.2	36.2	0.1	0.7	0.1	1.6	0.4	1.2	*15*	PAR2 plays a key role in chronic joint inflammation
Other Receptors													
Fc ε RI α (BC005912) 147138	Ba	19.4	219.0	4.6	5.5	1.4	5.1	0.8	1.4	0.4	0.2	*0*	responsible for initiating the allergic response
HTm4 (L35848) 606498	Ba	0.6	133.1	6.9	3.5	0.2	0.5	0.4	0.1	0.2	0.0	*1*	Cell cycle regulator
IL-3 R (NM_002183) **308385**	Ba	0.6	52.6	2.0	0.7	0.2	0.3	0.2	0.7	0.1	0.1	*0*	promotes the proliferation and differentiation of hematopoietic cells
CD244 NK cell R (NM_016382) 605554	Ba, Eo	0.3	56.0	16.5	1.2	0.1	0.4	3.5	5.2	1.1	0.1	*0*	engagement of 2B4 with specific antibody activates NK cytolytic activity
fibroblast growth factor R 2 (NM_022969) 176943	Ba, Eo	0.1	27.9	12.1	0.2	0.1	0.1	0.2	0.1	0.1	1.0	*17*	Receptor for acidic and basic fibroblast growth factors.
IL-5R α (M75914) **147851**	Ba, Eo	0.9	20.5	30.4	0.6	0.1	0.1	0.1	0.1	0.2	0.1	*0*	lacking either Il5ra or Sox4 have defects in B-cell development
Siglec 8 (NM_014442) 605639	Eo	1.8	0.3	17.4	0.4	0.3	0.2	0.1	0.2	0.5	0.2	*0*	SIGLEC8 expression on eosinophils but not other leukocytes
CD117 c-KIT (NM_000222) **164920**	MC	89.0	7.2	4.2	1.2	0.8	0.2	0.5	0.1	0.1	0.5	*15*	Signaling from the KIT receptor tyrosine kinase is essential for primordial germ cell growth both in vivo and in vitro
Siglec 6 (D86358) 604405	MC	5.6	0.2	0.0	0.2	0.5	0.0	0.0	0.0	0.4	0.0	*0*	OBBP1 is almost exclusively expressed on B cells.
Fc ε RIβ (NM_000139) 147138	MC, Ba	22.3	44.3	0.4	0.6	1.6	0.5	0.2	0.0	0.3	0.1	*0*	MS4A2 Allergic disease
low density lipoprotein R	MC, Ba	20.7	20.4	1.3	1.8	2.3	2.1	3.4	3.5	0.8	6.3	*34*	receptor-mediated endocytosis

Figure 3 D

(NM_000527) 606945 TRK neurotrophin R (NM_002529) 191315	MC, Ba	4.6	7.3	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	*0*	participates in the primary signal transduction mechanism of NGF; is also an immunoregulatory cytokine acting on monocytes
butyrophilin like R (AK025267)	Ne	1.1	1.7	1.5	6.9	1.5	1.7	1.6	0.9	1.5	1.3	*1*	his gene is mainly expressed in small intestine, colon, testis, and leukocytes
CD120a, TNF-R-I (NM_001065) 191190	Ne	1.7	1.2	7.8	74.7	1.3	2.2	5.9	17.4	0.6	16	*35*	Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate- specific cysteine proteases) mediating apoptosis. Contributes to the induction of noncytocidal TNF effects including anti-viral state and activation of the acid sphingomyelinase.
CD95, Fas, APO-1 (AA164751) **134637**	Ne	1.4	10.9	7.3	50.4	1.3	5.6	4.8	3.6	2.6	9.7	*7*	Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS- mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both. The secreted

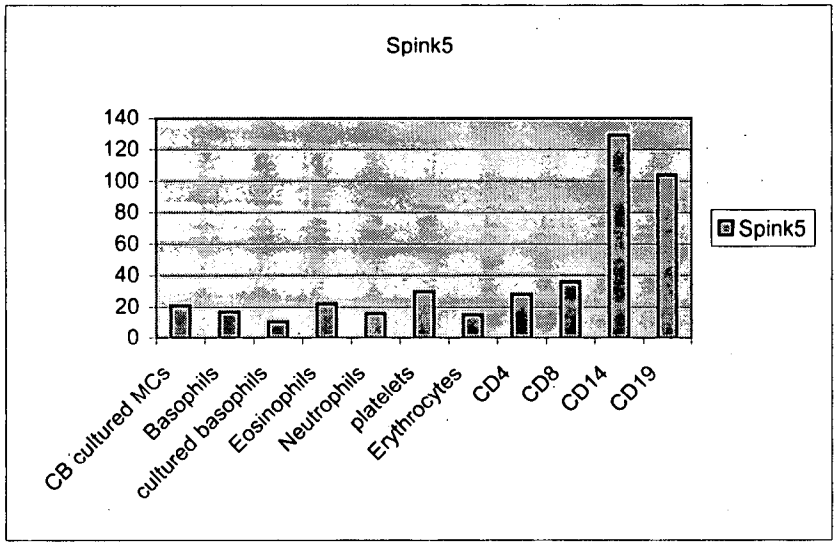
Figure 3 E

													isoforms 2 to 6 block apoptosis (in vitro).
decoy R1, TRAILR3 (AF012536) **603613**	Ne	0.1	1.5	7.7	78.7	0.5	0.2	0.1	0.7	0.1	0.6	*0*	does not induce apoptosis.
Fcγ R IIc2 (U90939)	Ne	1.5	2.4	7.8	59.9	0.3	0.2	0.1	7.2	2.3	0.2	*2*	
Fcγ R IIc3 (U90940)	Ne	2.4	10.7	10.0	84.3	3.0	1.4	0.6	14.0	7.2	1.0	*5*	
Fcγ R III (J04162) **146740**	Ne	0.7	1.6	1.9	199.6	6.6	1.3	1.3	2.2	2.6	0.1	*4*	failure of the patient's neutrophils to express Fc receptor III was associated with SLE
G-CSF R (NM_0007601) **138971**	Ne	0.1	0.4	1.6	163.6	0.2	0.8	0.2	25.5	0.1	0.2	*3*	inhibits cell proliferation and survival in response to CSF3
IL-13 R (U81379) 308385	Ne	0.3	0.2	2.0	14.1	0.4	0.4	0.3	2.9	1.3	1.3	*0*	romotes the proliferation and differentiation of hematopoietic cells
IL-1R, type II (NM_004633) 147811	Ne	0.1	0.1	0.1	53.5	0.2	0.4	0.1	0.2	0.0	0.0	*3*	type II receptor inhibits IL1 activity by acting as a decoy target for IL1
IGFR 1 (NM_000875) 147370	Ne	0.3	3.5	5.0	17.4	1.6	0.1	2.8	2.4	2.0	3.5	*3*	IGFs may elicit a myogenic event which may be a key mechanism in the etiology of breast and ovarian cancer
IGFR 2 (NM_000876) 147280	Ne	4.6	0.9	5.4	85.3	1.7	2.9	8.7	8.4	4.8	15	*32*	Mutation in either MPRD or MPRI might result in a clinical disorder resembling a mucolipidosis
leukocyte immunoglobulin-like R A2 (NM_006866) 604812	Ne	0.5	5.8	4.3	41.2	1.8	0.0	0.1	11.6	0.5	0.1	*2*	Eosinophils may be activated through LIR7 for release of eosinophil-derived neurotoxin
Toll-like R 1 (AL050262) 601194	Ne	0.6	0.3	1.2	31.5	1.6	0.8	0.7	3.0	1.5	0.3	*0*	that TLR2-TLR1 heterodimers mediated the strongest cell activation
Toll-like R 2 (NM_003264) 603028	Ne	0.9	6.0	1.3	83.8	1.6	1.3	0.1	26.3	0.9	0.4	*0*	TLR2 is a molecular link between microbial products, apoptosis, and host defense mechanisms
Toll-like R 6 (NM_006068)	Ne	0.5	1.0	0.9	8.8	0.1	0.9	0.9	2.1	1.2	0.6	*0*	immunostimulatory activity

a. Cell-type specificity was obtained by comparing the "normalized AD" levels of each gene in mast cells (MC; average of 2 experiments), basophils (Ba; average of 3 experiments), eosinophils (Eo; average of 4 experiments), neutrophils (Ne; average of 4 experiments), platelets (Pl), $CD4^+$ cells (CD4), $CD8^+$ cells (CD8), $CD14^+$ cells (CD14), CD19+ cells (CD19) and nasal polyp-derived cultured fibroblasts (Fb).

	CB cultured MCs	Basophils	cultured basophils	Eosinophils	Neutrophils	platelets	Erythrocytes	CD4	CD8	CD14	CD19
Spink5	21	17	11	22	16	30	15	28	36	129	104
chymase human	1221	47	65	45	12	101	62	108	59	104	45
tryptase alpha	21179	212	40	33	25	184	139	104	17	52	39
tryptase beta	25414	195	113	49	28	152	10	122	113	93	6
tryptase delta	349	45	6	23	55	74	113	11	10	42	11
tryptase gamma	654	56	19	38	78	28	24	81	230	142	83
TRPV2	129	37	15	97	99	259	137	133	67	97	110
ANKTM1	28	28	8	38	30	96	18	14	46	11	28
Cannabinoid receptor type I	50	41	14	47	36	27	61	41	56	18	54
Cannabinoid receptor type 2	160	369	226	578	177	271	530	324	232	212	421

Figure 4A


Spink5
140
120
100
80
60
40
20
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
Spink5

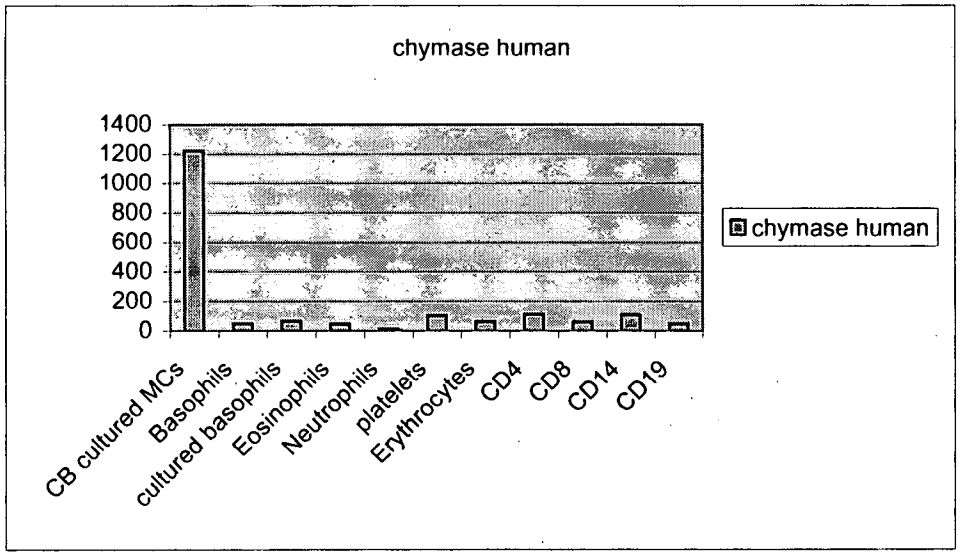
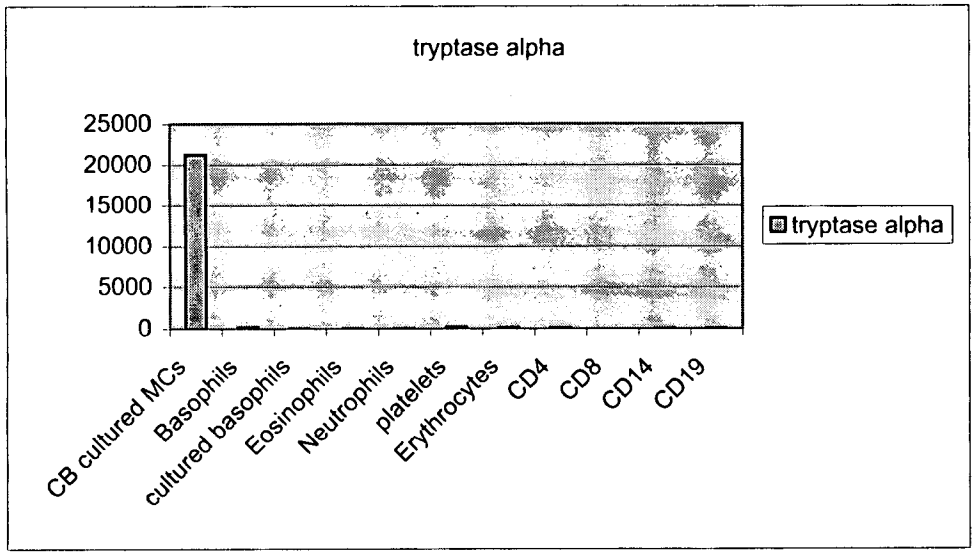

chymase human
1400
1200
1000
800
600
400
200
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
chymase human

Figure 4B


tryptase alpha
25000
20000
15000
10000
5000
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
tryptase alpha

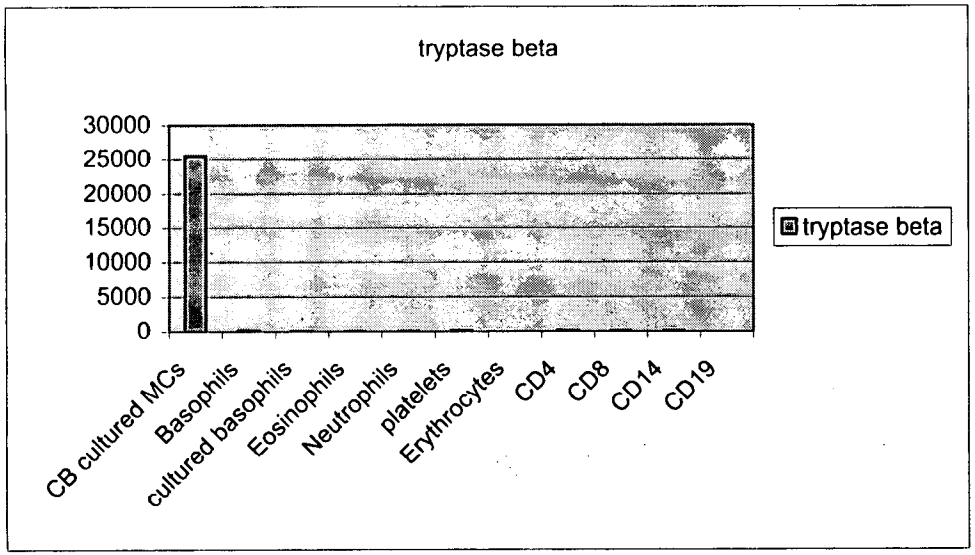
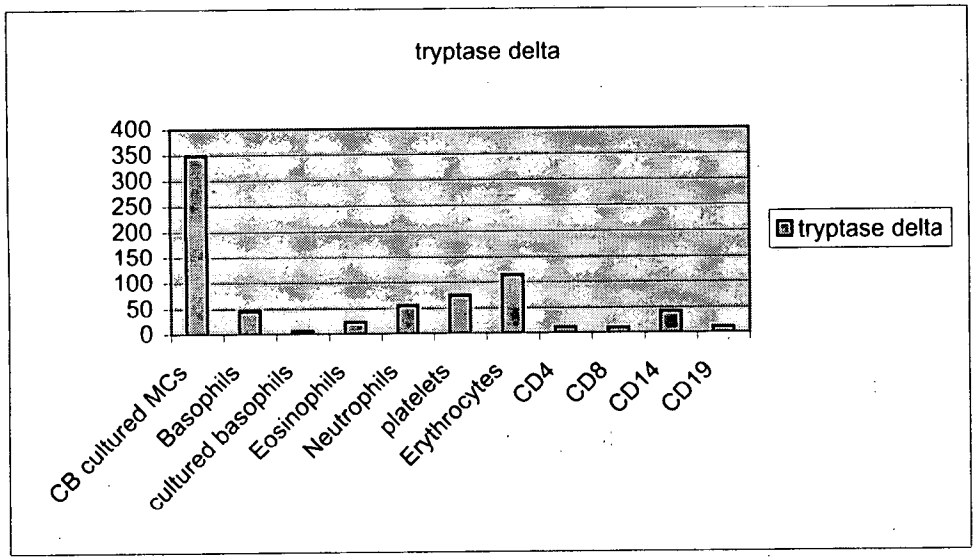

tryptase beta
30000
25000
20000
15000
10000
5000
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
tryptase beta

Figure 4C


tryptase delta
400
350
300
250
200
150
100
50
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
tryptase delta

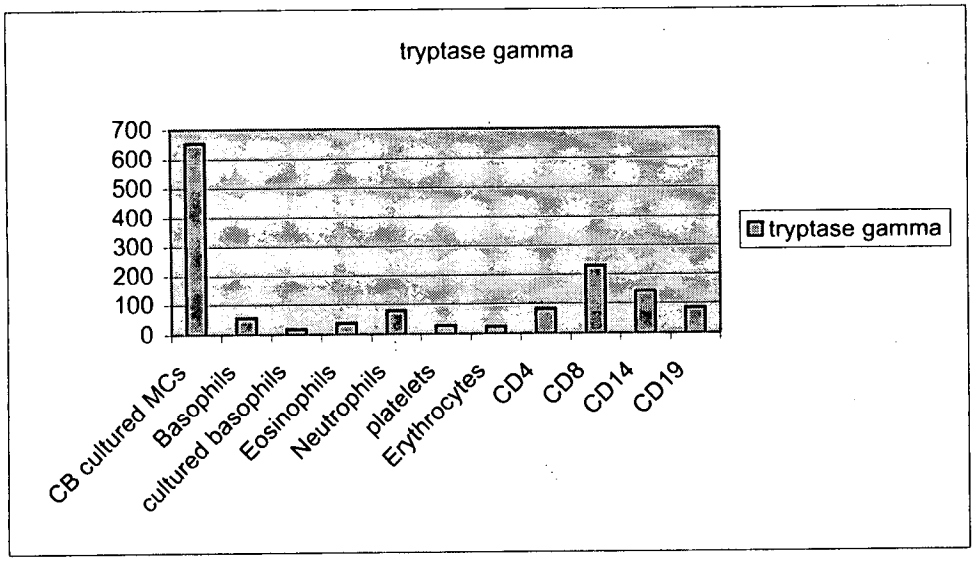
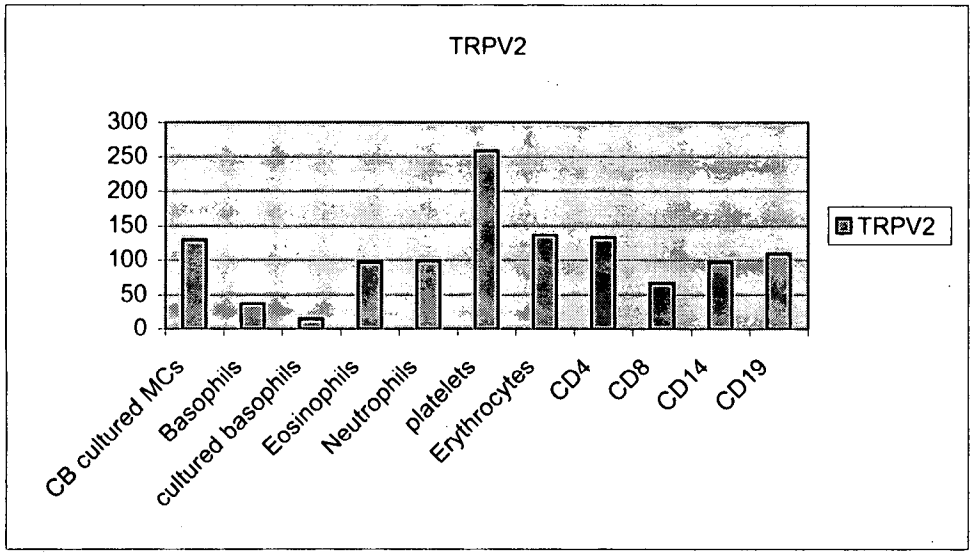

tryptase gamma
700
600
500
400
300
200
100
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
tryptase gamma

Figure 4 D


TRPV2
300
250
200
150
100
50
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
TRPV2

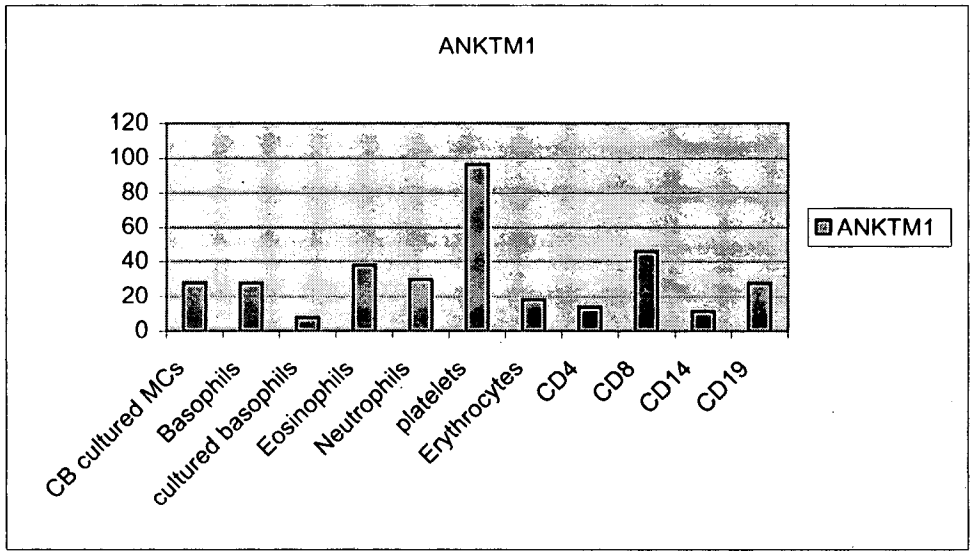
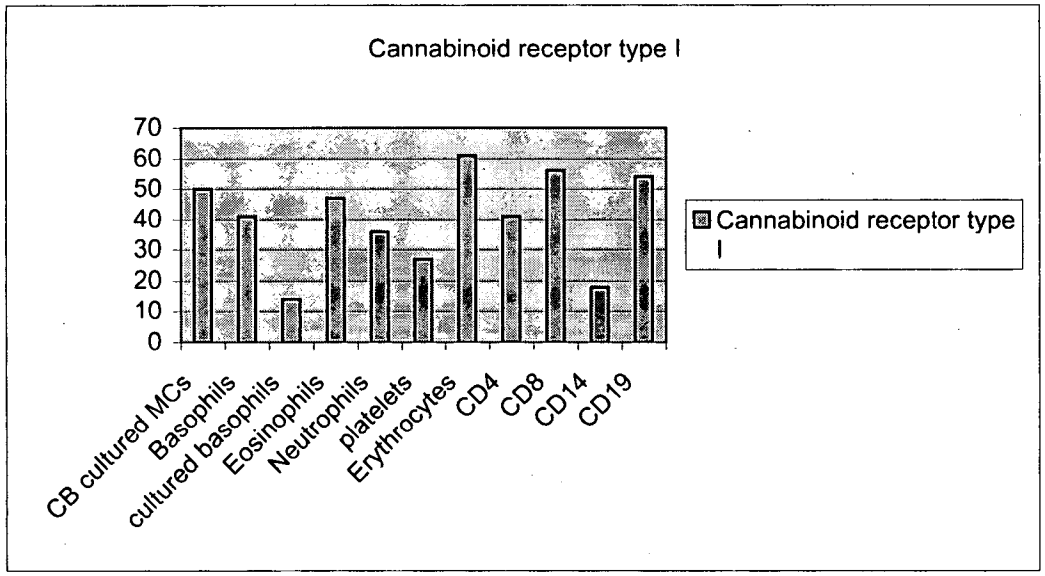

ANKTM1
120
100
80
60
40
20
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
ANKTM1

Figure 4E


Cannabinoid receptor type I
70
60
50
40
30
20
10
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
Cannabinoid receptor type I

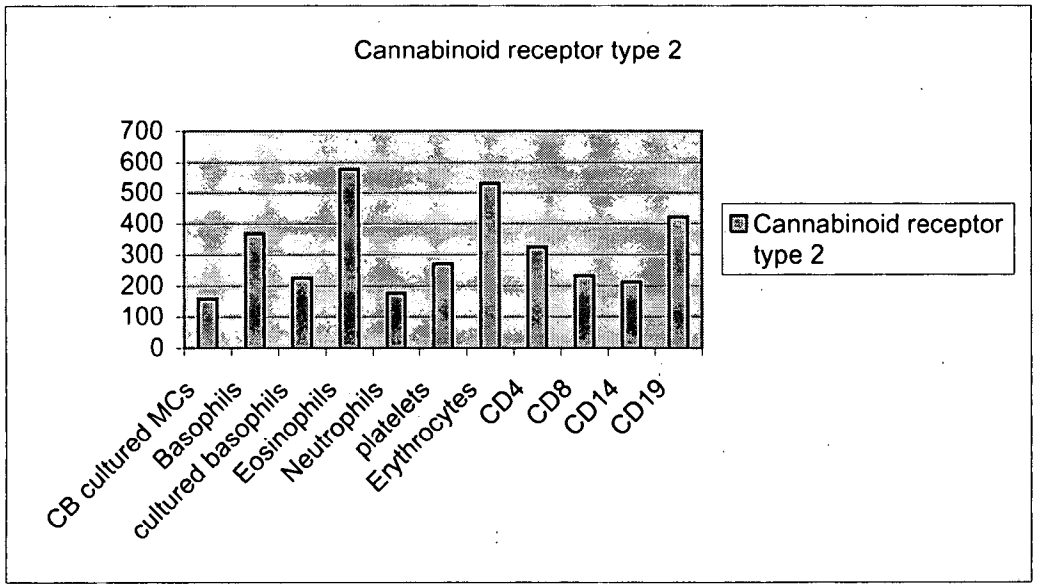
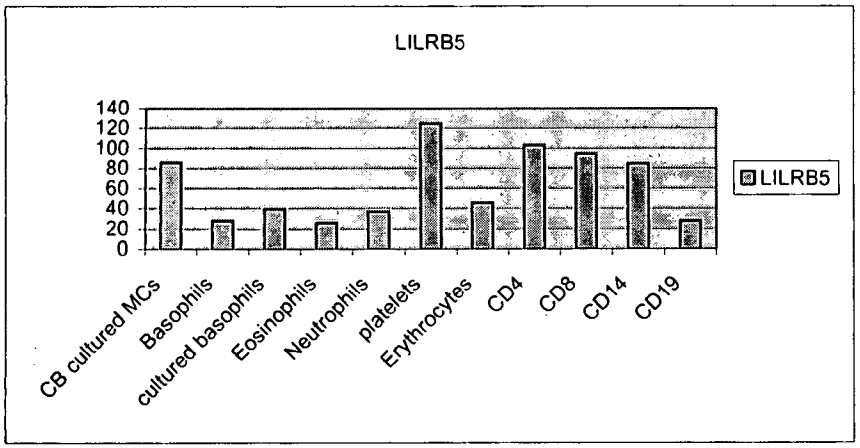
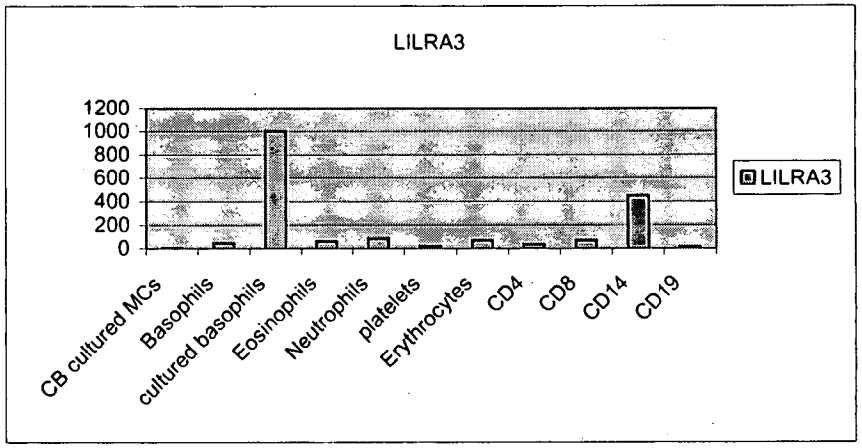

Cannabinoid receptor type 2
700
600
500
400
300
200
100
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
Cannabinoid receptor type 2

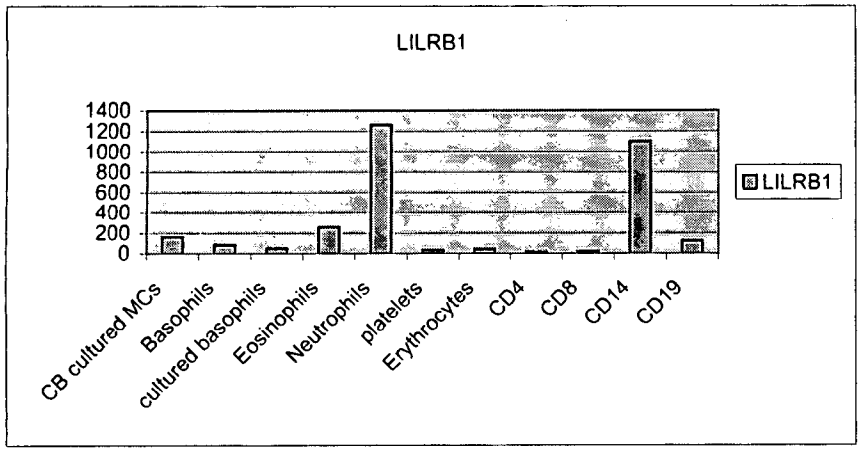
Figure 4F

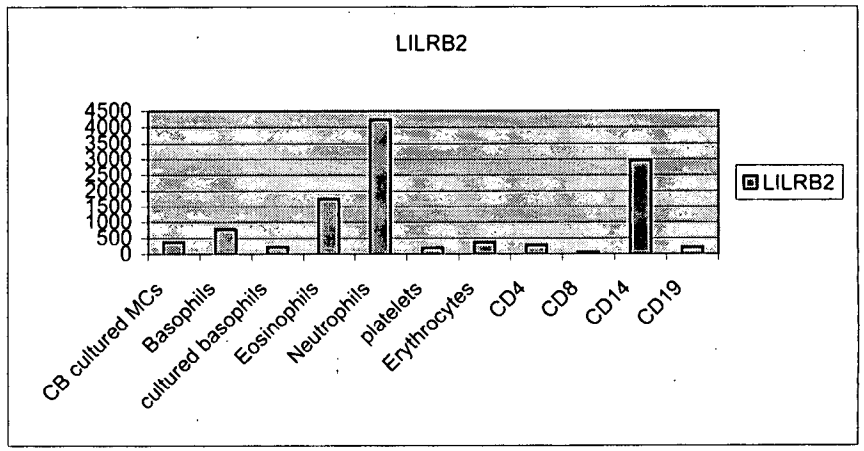
	CB cultured MCs	Basophils	cultured basophils	Eosinophils	Neutrophils	platelets	Erythrocytes	CD4	CD8	CD14	CD19	
LILRB5	86	28	39	26	37	125	46	103	95	85	28	
LILRA3	4	45	1004	59	84	18	68	31	68	451	13	
LILRB1	165	84	51	258	1261	31	42	13	18	1105	125	
LILRB2	375	780	227	1755	4237	199	375	286	58	2963	214	
LILRA2	49	614	384	461	3269	146	318	8	9	1247	52	
LILRA1	28	50	45	154	389	120	148	127	35	539	86	
KIR3DL2	7	58	34	18	23	13	106	14	286	68	204	
KIR2DS3	22	17	21	27	28	35	11	28	110	88	111	
KIR2DL3 variant	30	54	134	66	61	149	95	39	247	147	271	
KIR2DS1	35	138	81	88	93	191	132	57	257	21	267	
KIR2DS5	24	31	23	21	21	53	27	33	135	19	173	
KIR2DL4	139	140	85	157	144	280	210	35	239	152	196	
KIR2DL4	11	45	41	50	41	88	15	19	72	77	85	
KIR-123FM	41	43	31	20	52	31	121	96	163	26	193	
KIR2DL5.3	27	83	24	41	49	61	239	92	323	56	72	
KIR3DL1	68	89	41	51	95	75	97	76	169	36	196	
MIR cl-10	144	621	83	1334	2386	107	146	145	52	2154	99	
PTPRF	18	14	5	28	37	86	12	13	14	32	23	

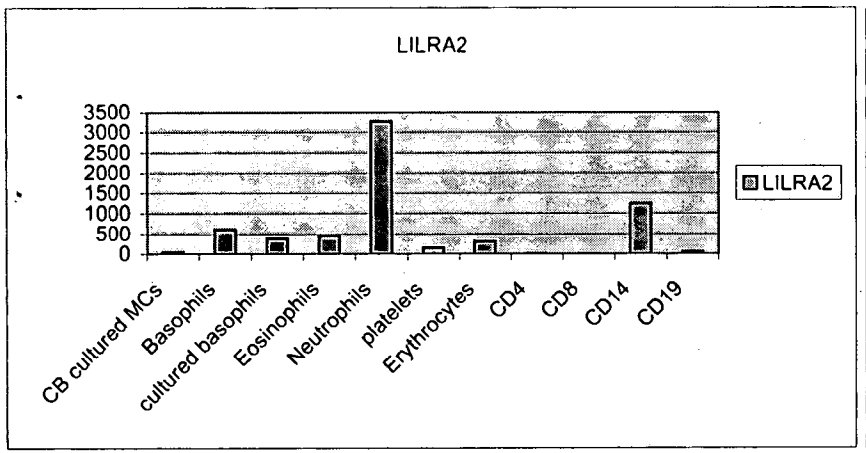
Figure 5A


LILRB5
140
120
100
80
60
40
20
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
LILRB5


LILRA3
1200
1000
800
600
400
200
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
LILRA3


LILRB1
1400
1200
1000
800
600
400
200
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
LILRB1


LILRB2
4500
4000
3500
3000
2500
2000
1500
1000
500
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
LILRB2


LILRA2
3500
3000
2500
2000
1500
1000
500
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
LILRA2

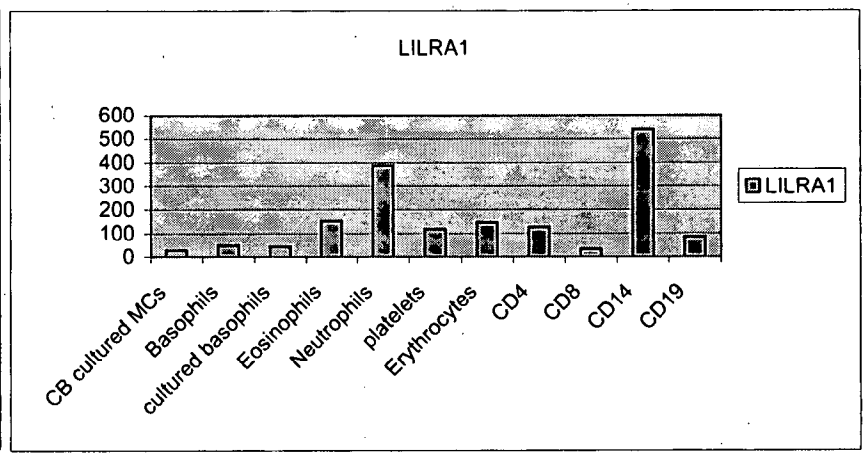
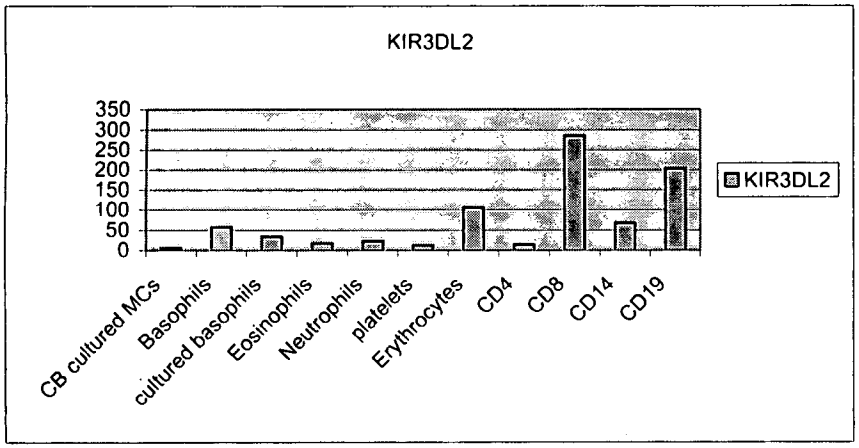
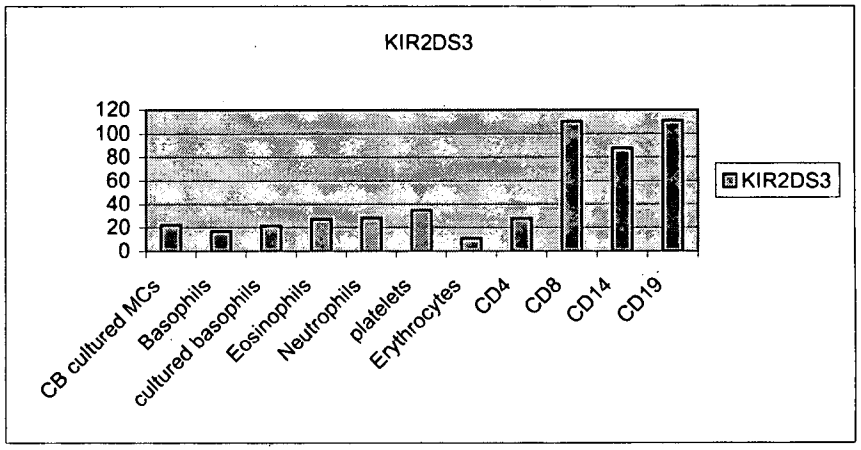
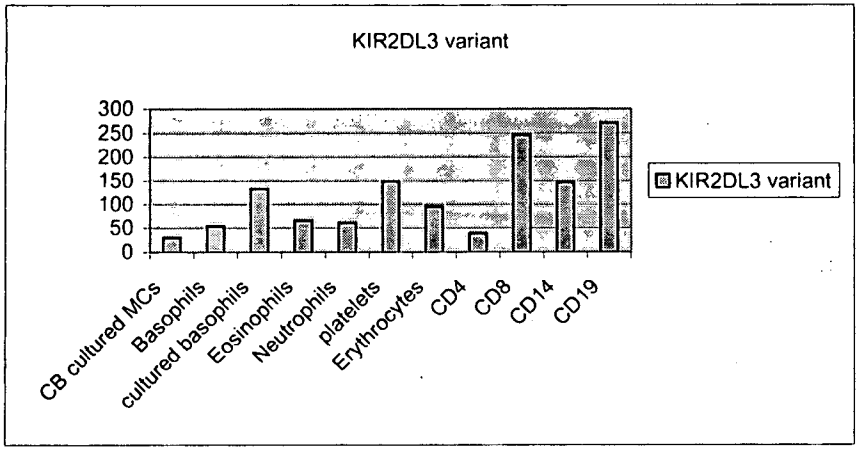
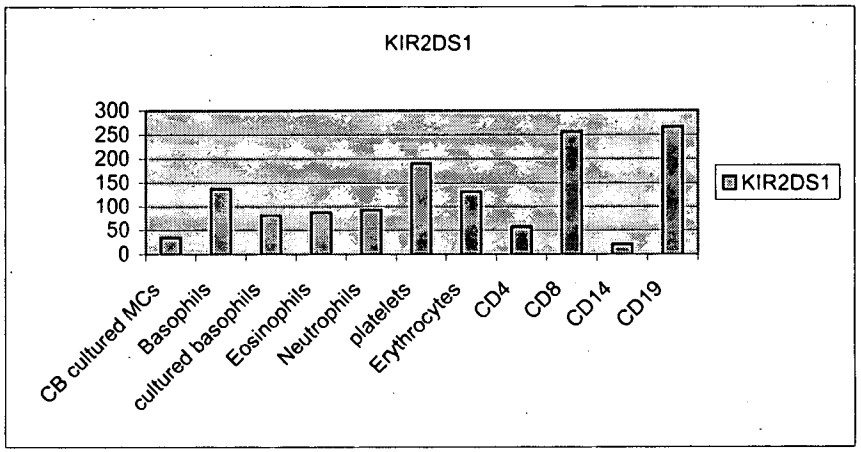

LILRA1
600
500
400
300
200
100
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
LILRA1

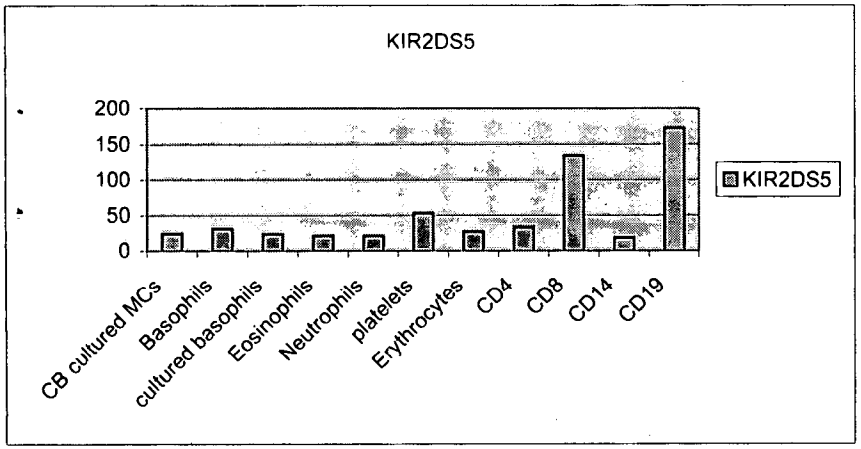
Figure 5B

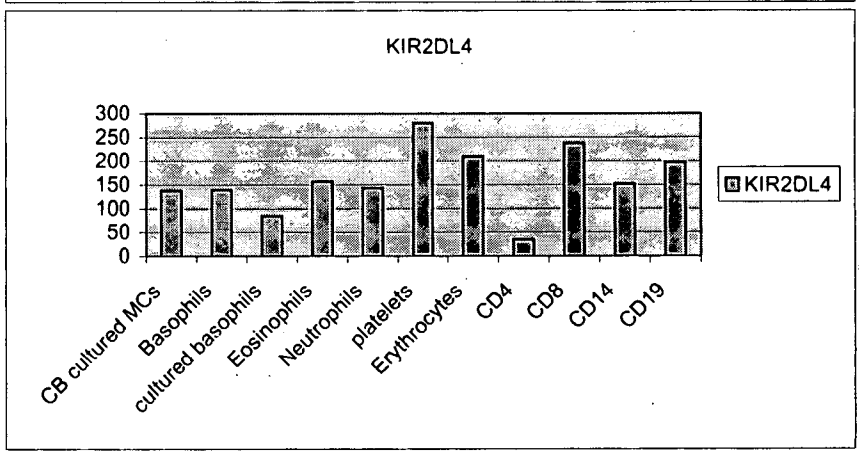

KIR3DL2
350
300
250
200
150
100
50
0
KIR3DL2
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19


KIR2DS3
120
100
80
60
40
20
0
KIR2DS3
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19


KIR2DL3 variant
300
250
200
150
100
50
0
KIR2DL3 variant
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19


KIR2DS1
300
250
200
150
100
50
0
KIR2DS1
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19


KIR2DS5
200
150
100
50
0
KIR2DS5
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19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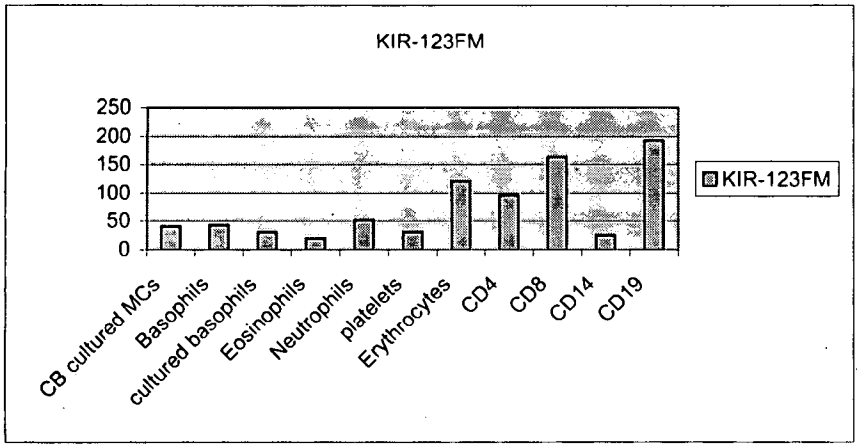
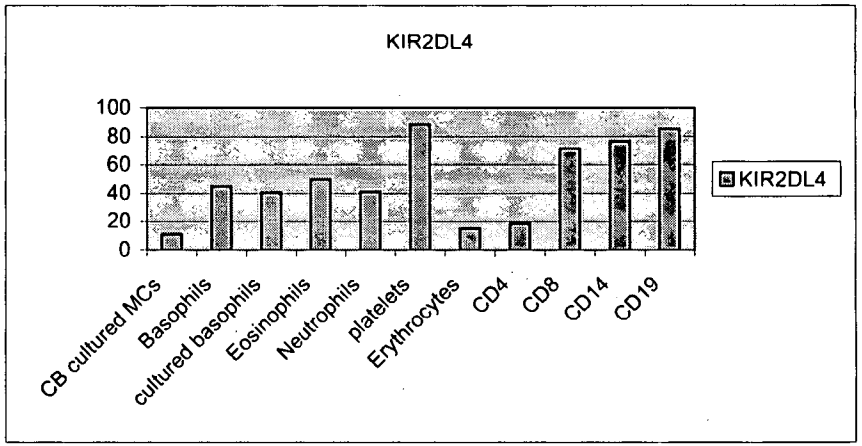
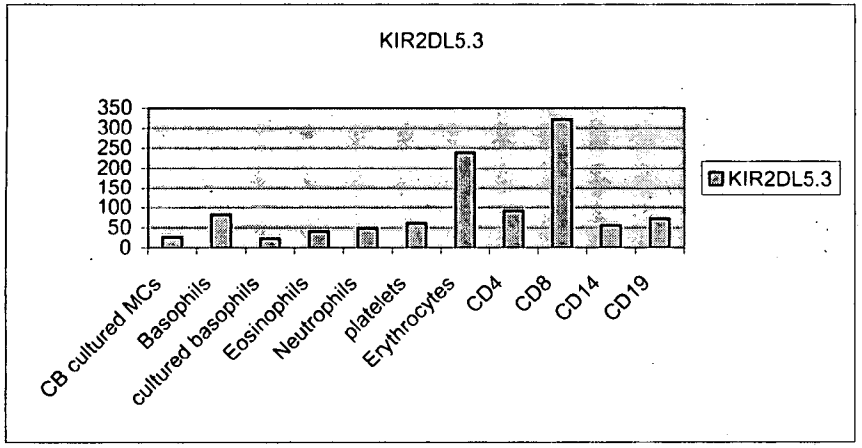
250
200
150
100
50
0
KIR2DL4
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19

Figure 5C


KIR-123FM
250
200
150
100
50
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
KIR-123FM


KIR2DL4
100
80
60
40
20
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
KIR2DL4


KIR2DL5.3
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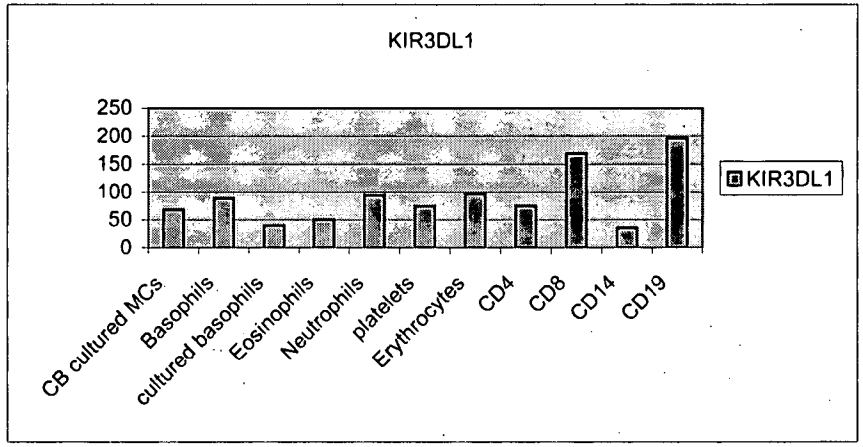
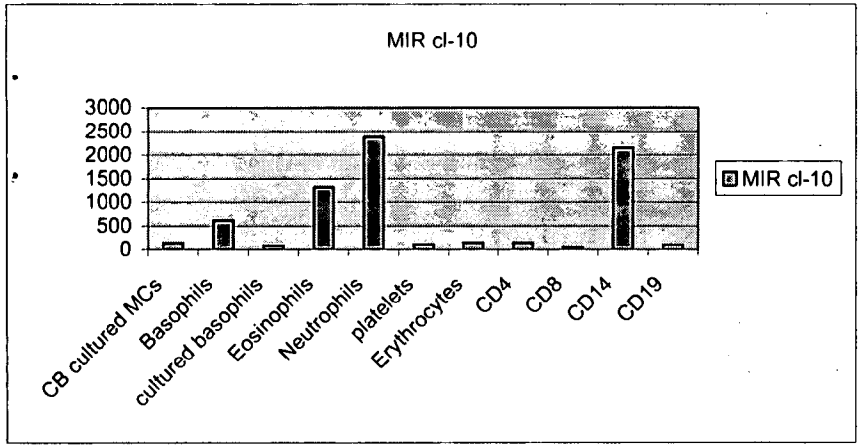
300
250
200
150
100
50
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
KIR2DL5.3


KIR3DL1
250
200
150
100
50
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
KIR3DL1


MIR cl-10
3000
2500
2000
1500
1000
500
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
MIR cl-10

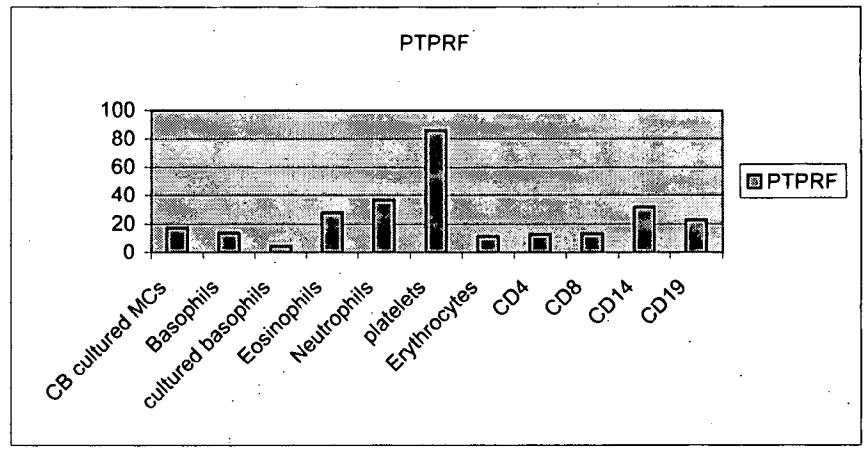

PTPRF
100
80
60
40
20
0
CB cultured MCs
Basophils
cultured basophils
Eosinophils
Neutrophils
platelets
Erythrocytes
CD4
CD8
CD14
CD19
PTPRF

Figure 5D

Table E1. The complete list of granulocyte subtype-selective transcripts. Selectivity index (S.I.) was calculated by comparing the "normalized AD" level of a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types including platelets (Pl), $CD4^+$ cells, $CD8^+$ cells, $CD14^+$ cells, $CD19^+$ cells and nasal polyp-derived cultured fibroblasts (Fb). When the result was accompanied by presence call, it was shown as a bold numeral. Italic numerals show that the raw AD levels were associated with absence call by the GeneChip analysis software. Transcripts having S.I. >3-fold were shown in A-H. Abbreviations used in the table through A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

A. Basophil (Ba)-selective transcripts (1/2).

Probe set	Accession #		Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba S.I.
207539_s_at	NM_000589.1		IL-4	*0.2*	*0.1*	**10.4**	**16.9**	**13.4**	*0.1*	*0.0*	*0.2*	*0.1*	*0.1*	*0.3*	*0.0*	*1.2*	*0.2*	*0.0*	*0.2*	*0.1*	*0.0*	*0.0*	73.348
210254_at	L35848.1	R	HTm4	*0.8*	*0.4*	**115.6**	**130.1**	**153.6**	**2.4**	*1.7*	**21.8**	**1.7**	*0.1*	*0.9*	**3.6**	**9.5**	*0.2*	*0.5*	*0.4*	*0.1*	*0.2*	*0.0*	38.24
205513_at	NM_001062.1		vitamin B12 binding protein	**1.5**	*1.2*	**98.9**	**149.3**	**110.9**	**3.2**	*2.2*	**16.1**	*1.9*	**4.9**	**4.5**	**6.3**	**8.1**	*1.8*	*0.7*	*0.8*	*1.4*	*0.9*	*0.1*	20.322
206148_at	NM_002183.1	R	IL-3 R	*1.0*	*0.1*	**6.2**	**80.2**	**71.3**	*1.7*	*1.7*	*1.8*	**2.9**	*0.3*	*0.4*	*0.2*	*1.9*	*0.2*	*0.3*	*0.2*	*0.7*	*0.1*	*0.1*	16.62
214920_at	R33964		FLJ11022 fis	*0.1*	*1.1*	**4.9**	**13.1**	**15.4**	*0.1*	*0.2*	*0.7*	**0.5**	*1.0*	*0.4*	*0.5*	*0.7*	*0.1*	*0.1*	*0.2*	*0.1*	*0.3*	*0.1*	16.049
201825_s_at	AL572542		CGI-49	**3.3**	**1.6**	**21.4**	**74.9**	**46.5**	**2.1**	*1.2*	*0.1*	*1.2*	*0.1*	*0.1*	*0.2*	*0.1*	*1.3*	*0.7*	**1.7**	*1.4*	*0.8*	**2.8**	15.045
213238_at	AI478147		ATPase, Class V, type 10D	**1.2**	**2.9**	**39.9**	**76.3**	**118.9**	*2.3*	**1.7**	**3.1**	**1.9**	*2.1*	*1.4*	**2.3**	**6.8**	*0.7*	*0.9*	*0.9*	**2.5**	**5.0**	**4.1**	14.398
211734_s_at	BC005912.1	R	Fc epsilon R I alpha	**10.5**	**28.4**	**210.0**	**220.8**	**226.2**	**8.4**	**2.1**	**4.8**	**2.9**	*0.3*	*0.7*	**4.5**	**16.6**	**1.4**	**5.1**	**0.8**	**1.4**	*0.4*	*0.2*	12.703
213894_at	BF447246		KIAA0960	*0.1*	*0.0*	**3.7**	**13.0**	**15.6**	*0.3*	*0.4*	*0.4*	*0.4*	*0.9*	*0.7*	*0.7*	*0.6*	*0.5*	*0.6*	*0.1*	*0.1*	*0.2*	*0.2*	12.272
206363_at	NM_005360.2		c-MAF	**3.7**	*1.4*	**36.5**	**75.7**	**66.4**	*1.2*	*0.1*	*0.2*	*0.2*	*0.2*	*0.1*	*0.2*	*1.0*	*0.6*	**4.8**	**2.7**	*0.5*	*1.0*	*0.0*	11.927
203373_at	NM_003877.1		SOCS2	**2.1**	**3.9**	**21.7**	**85.0**	**112.2**	**4.6**	**4.7**	**9.4**	**6.5**	*0.7*	*1.2*	*0.3*	**2.5**	*1.6*	**3.2**	**3.5**	*0.8*	*0.9*	**3.6**	9.8282
207538_at	*NM_000589.1*		*IL-4*	*0.3*	*0.1*	**5.4**	**9.8**	**9.2**	*0.4*	*0.4*	*0.0*	*0.3*	*0.1*	*0.0*	*0.4*	*0.7*	*0.8*	*0.4*	*0.3*	*0.1*	*0.0*	*0.1*	9.8156
213684_s_at	BF671400		LIM-protein	*0.6*	*0.1*	**11.1**	**21.0**	**20.6**	**1.9**	*1.6*	**2.4**	**1.8**	*0.8*	*0.6*	**1.5**	**2.5**	*0.1*	*0.0*	*0.3*	*1.0*	*0.0*	*0.1*	8.9245
209360_s_at	D43968.1		AML1b protein	**10.4**	*2.4*	**53.2**	**131.1**	**90.5**	**8.5**	**7.0**	**13.8**	**11.3**	*0.5*	*0.5*	*0.5*	*4.2*	*1.3*	*4.1*	**5.9**	*1.3*	*2.5*	**3.1**	8.7543
220234_at	NM_004056.2		carbonic anhydrase VIII	*0.4*	*0.1*	**11.7**	**10.2**	**6.0**	*1.2*	*0.1*	*0.2*	*0.4*	*0.8*	*0.9*	*0.1*	*0.5*	*0.5*	*1.1*	*0.1*	*0.1*	*0.8*	*0.0*	8.1309
210643_at	AF053712.1		osteoprotegerin ligand	*0.1*	*0.3*	**1.8**	**3.4**	**6.0**	*0.7*	*0.4*	*0.3*	*0.2*	*0.4*	*0.1*	*0.3*	*0.1*	*0.1*	*0.3*	**0.4**	*0.3*	*0.2*	*0.2*	7.6628
209211_at	AF132818.1		colon Kruppel-like factor	*0.1*	*0.0*	**1.8**	**10.2**	**8.8**	*0.3*	*0.5*	**1.5**	**0.8**	*1.1*	*0.7*	*0.8*	*0.5*	*0.2*	*0.2*	*0.4*	*0.2*	*0.1*	*0.3*	7.239
204309_at	NM_000781.1		CYP11A	*0.3*	*0.1*	**2.6**	**6.1**	**5.6**	*0.1*	*0.3*	*0.5*	*0.5*	*1.0*	*0.1*	*0.1*	*0.9*	*0.3*	*0.3*	*0.1*	*0.0*	*0.3*	**0.7**	6.8366
203372_s_at	AB004903.1		*SOCS2*	0.6	*1.6*	**9.2**	**8.5**	**15.9**	**1.4**	**2.4**	**0.9**	*0.2*	*0.7*	*0.6*	*0.4*	*0.8*	*0.8*	**1.6**	**1.3**	*0.3*	*0.3*	**1.4**	6.8271
207463_x_at	NM_002771.1		serine protease 3 (trypsin 3)	*1.0*	*1.0*	**4.8**	**10.0**	**10.9**	*0.4*	*1.0*	**1.0**	*1.2*	*1.2*	*0.9*	*1.0*	**1.8**	*0.4*	*0.6*	*0.4*	*0.3*	*0.7*	**1.2**	6.7218
213624_at	AA873600		acid sphingomyelinase-like phosphodiesterase	**4.7**	**2.0**	**20.8**	**30.6**	**25.9**	**2.1**	**2.8**	**3.8**	**1.7**	*0.5*	**1.1**	**1.3**	1.3	*0.1*	*0.2*	*0.1*	**3.8**	*0.2*	**3.2**	6.6846
214873_at	AL137651.1		clone DKFZp434O0213	*0.1*	*0.4*	**3.7**	**15.5**	**24.4**	*2.0*	*0.9*	*2.5*	*2.3*	*0.2*	*0.1*	*0.7*	*0.6*	*0.1*	*1.1*	**1.5**	*0.5*	*0.6*	*0.7*	6.2585
204928_s_at	NM_019848.2		protein P3	**2.3**	**1.5**	**9.8**	**49.0**	**34.3**	**3.7**	**3.3**	**4.8**	**4.2**	*1.6*	*1.0*	**1.9**	2.2	*4.1*	*1.8*	**3.0**	*0.8*	**2.0**	**2.6**	6.2142
208935_s_at	L78132.1		prostate carcinoma tumor antigen (pcta-1)	**2.2**	*1.2*	**9.9**	**19.1**	**16.6**	**2.3**	**1.5**	**3.6**	**2.5**	**1.1**	**1.1**	**1.9**	*0.9*	**1.8**	**1.8**	**2.0**	**2.0**	*1.4*	**0.8**	6.2011
203201_at	NM_000303.1		phosphomannomutase 2 (PMM2)	**1.8**	*0.3*	**10.7**	**15.9**	**6.5**	*0.9*	*0.6*	*1.2*	*0.9*	*0.8*	*0.4*	*1.1*	**1.3**	**1.0**	1.3	**1.2**	**1.2**	**1.1**	**1.7**	6.1557
201826_s_at	NM_016002.1		*CGI-49*	**1.8**	**3.1**	**11.0**	**27.5**	**15.1**	*1.6*	*1.1*	*1.4*	**2.1**	*1.1*	*1.4*	*1.3*	*1.8*	*1.6*	*1.1*	*1.1*	*1.1*	*0.6*	**2.9**	5.6407
213421_x_at	AW007273		serine protease 4 (trypsin 4)	**1.8**	**1.7**	**5.9**	**12.5**	**11.4**	*1.0*	*0.5*	**1.2**	*0.5*	*1.2*	**1.7**	**1.2**	**1.2**	*0.9*	**1.0**	*1.2*	*1.0*	*0.4*	**1.7**	5.4802
209348_s_at	AF055376.1		*c-MAF, short form*	**6.4**	**4.9**	**29.6**	**47.7**	**42.3**	**0.8**	*0.3*	*0.4*	*0.6*	*0.3*	*0.0*	*0.9*	**1.4**	*1.0*	**7.3**	**3.1**	**0.9**	**0.7**	**1.4**	5.3183
213343_s_at	AL041124		hypothetical protein PP1665	*0.9*	*0.2*	**12.2**	**17.0**	**12.0**	**3.5**	*1.7*	*0.5*	*0.6*	*0.1*	*0.3*	*0.8*	*0.4*	*0.6*	*1.5*	*2.6*	*0.7*	*1.6*	*1.3*	5.2721
202491_s_at	NM_003640.1		I kappa B-associated protein	**1.6**	**3.8**	**23.9**	**51.9**	**43.5**	**4.6**	**4.0**	**7.1**	**7.3**	*1.6*	**2.1**	**2.5**	**2.3**	*1.7*	**3.7**	**7.4**	**3.2**	**4.7**	**4.2**	5.107
221021_s_at	NM_030877.1		Bos taurus P14 protein	**6.9**	**3.2**	**7.2**	**29.2**	**58.9**	**2.8**	**3.2**	**5.4**	**6.3**	*0.9*	*1.2*	*1.8*	**1.6**	*1.6*	**2.2**	**2.4**	**2.0**	**3.5**	1.8	4.9129
213346_at	BE748563		hypothetical protein BC015148	**2.7**	**1.8**	**17.5**	**38.8**	**25.8**	**4.0**	**6.7**	**6.2**	**4.8**	*1.4*	*0.9*	*0.8*	*1.1*	*0.2*	*1.2*	*1.5*	*0.6*	*1.1*	**1.9**	4.8879
209764_at	AL022312		mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	*0.0*	*0.9*	**4.1**	**6.1**	**5.8**	*0.8*	*1.4*	0.9	*1.4*	*0.6*	*0.1*	*0.5*	*0.2*	*1.0*	*0.4*	*0.2*	*0.2*	*0.4*	*0.3*	4.855
207067_s_at	NM_002112.1		histidine decarboxylase	**64.1**	**14.7**	**105.2**	**164.9**	**165.7**	**3.4**	*1.4*	**4.1**	*2.8*	*2.1*	*1.2*	*4.6*	**14.0**	*2.4*	*0.8*	*0.9*	*1.1*	*0.7*	*0.2*	4.6305
210375_at	X83858.1	GPR	prostaglandin E receptor, type 3a2	*1.0*	*0.6*	**2.4**	**11.5**	**17.0**	*0.3*	*0.1*	*0.1*	*0.0*	*0.4*	*0.7*	*0.9*	*0.7*	*0.6*	*0.3*	*0.2*	*0.2*	*0.5*	**1.7**	4.6103
206306_at	NM_001036.1		ryanodine receptor 3 (RYR3)	**2.1**	*1.1*	**3.7**	**11.0**	**7.8**	**1.0**	**0.6**	**1.5**	0.5	**1.2**	*0.3*	**1.5**	**0.9**	**1.1**	*0.7*	*0.3*	**1.0**	*0.2*	**0.4**	4.5552
210001_s_at	AB005043.1		SOCS1	**5.2**	*0.2*	**3.0**	**24.1**	**29.9**	**2.1**	**3.0**	**3.2**	**3.4**	*0.3*	*1.0*	0.8	**1.3**	*0.8*	*0.8*	*0.8*	*0.0*	*0.8*	**0.9**	4.5248
204614_at	NM_002575.1		serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2 (SERPINB2)	*0.3*	*0.6*	**5.3**	**12.9**	**12.5**	*0.4*	**2.4**	**4.2**	**2.0**	*1.0*	*0.8*	*0.7*	*0.3*	**1.9**	*0.5*	*0.7*	**2.1**	*0.2*	*0.2*	4.5061
209960_at	X16323.1		hepatocyte growth factor (HGF)	*0.4*	*0.0*	**2.3**	**7.3**	**5.5**	*0.5*	*0.4*	*0.6*	*0.5*	*0.1*	*0.1*	*1.0*	*0.6*	*0.7*	*0.1*	*0.0*	**1.0**	*0.0*	**0.5**	4.4335
209212_s_at	AB030824.1		transcription factor BTEB2	*0.1*	*0.2*	**7.5**	**14.3**	**22.1**	**2.3**	**2.0**	**4.9**	**3.7**	*1.2*	1.3	**1.5**	**2.5**	*1.4*	*0.5*	*0.2*	**1.1**	*0.9*	**0.8**	4.363

Figure 6A

A. Basophil (Ba)-selective transcripts (2/2).

Probe set	Accession #		Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba S.I.
214651_s_at	U41813.1		class I homeoprotein (HOXA9)	0.6	0.6	1.7	6.3	8.3	0.3	0.5	0.8	0.5	0.1	0.1	0.5	1.0	1.0	0.1	0.1	0.3	0.1	0.1	4.3618
32502_at	AL041124		DKFZp434D0316_s1	1.6	1.9	14.6	22.5	17.4	4.0	2.1	0.7	1.4	1.1	1.0	0.4	0.4	2.3	2.5	4.1	2.5	2.3	1.8	4.3594
205373_at	NM_004389.1		catenin (cadherin-associated protein), alpha 2	0.2	0.1	1.1	3.9	3.2	0.6	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.6	0.2	0.2	0.2	4.2308
219676_at	NM_025231.1		FLJ22191	0.3	0.7	2.5	7.3	12.0	0.9	0.2	2.0	1.5	0.2	1.1	4.2	2.2	0.6	1.1	1.4	0.3	1.4	0.1	4.2135
213385_at	AK026415.1		beta2-chimaerin	4.7	3.1	8.3	22.9	21.8	1.1	0.8	0.9	1.0	0.2	1.5	0.8	1.0	0.1	0.9	1.6	3.3	0.2	0.4	4.2131
214637_at	BG437034		oncostatin M	0.4	0.0	0.9	5.4	4.4	0.2	0.7	0.1	0.7	0.5	1.8	0.2	1.1	0.4	0.1	0.1	0.2	0.1	0.0	4.1983
202490_at	AF153419.2		*I kappa B-associated protein*	0.2	0.2	1.3	3.6	2.2	0.4	0.4	0.5	0.1	0.3	0.0	0.2	0.0	0.3	0.3	0.5	0.2	0.4	0.2	4.1747
220416_at	NM_024837.1		FLJ21472	4.1	1.5	9.1	9.7	12.2	1.9	3.3	3.0	1.9	0.8	0.6	1.1	0.9	0.7	0.6	0.2	0.8	0.3	0.0	4.1718
218318_s_at	NM_016231.1		nemo-like kinase	1.4	1.3	6.2	7.0	7.1	0.8	0.9	0.8	0.6	0.5	1.0	0.1	0.1	1.6	1.3	0.9	1.2	1.1	0.4	4.1558
215201_at	AW166925		FLJ14135 fis, clone MAMMA1002728	0.1	0.1	2.1	3.5	5.1	0.5	0.7	0.8	0.9	0.0	0.1	0.1	0.1	0.5	0.3	0.8	0.4	0.5	0.1	4.1491
222303_at	AV700891		ETS2 intronic transcript 1 mRNA	0.6	1.4	31.1	86.8	63.8	3.6	2.2	2.9	3.2	10.8	10.5	16.6	19.0	1.2	0.7	0.7	8.1	0.3	0.8	4.0555
201664_at	AL136877.1		DKFZp434F205	2.8	5.0	17.3	27.7	31.8	4.4	5.3	9.1	8.3	4.3	3.9	5.7	5.5	0.1	4.8	4.2	2.5	4.1	4.8	3.8471
210252_s_at	AB002356.1		MAP-kinase activating death domain	5.6	4.6	12.7	35.0	40.7	6.2	6.1	7.0	8.3	2.2	1.3	1.9	3.3	5.2	2.7	5.4	3.0	3.5	1.1	3.8424
201328_at	AL575509		v-ets avian erythroblastosis virus E26 oncogene homolog 2	1.7	0.1	18.4	34.7	50.7	2.8	1.6	1.7	1.8	6.4	9.9	8.7	8.9	0.5	0.9	1.0	4.4	0.1	1.7	3.8075
218392_x_at	NM_022754.1		FLJ12876	1.2	1.0	3.5	7.5	7.4	1.4	1.0	2.7	1.5	1.0	0.6	0.9	0.1	0.9	1.4	0.4	0.7	0.5	1.4	3.7693
205046_at	NM_001813.1		FLJ14150 fis, clone MAMMA1003026	0.0	0.3	1.5	8.1	13.1	1.7	0.5	1.9	1.2	0.5	1.3	1.0	0.9	1.1	1.5	0.9	1.0	0.4	0.2	3.7324
221170_at	AF312230.1	GPR	histamine H4 receptor	0.6	0.8	35.9	34.2	32.5	7.8	11.9	8.7	9.3	0.2	0.8	0.8	1.0	0.4	0.8	0.5	0.6	0.0	0.1	3.6719
201663_s_at	NM_005496.1		chromosome-associated polypeptide C	2.2	4.3	17.6	15.1	18.1	3.4	6.6	4.9	4.2	4.0	3.7	2.2	2.7	1.7	4.1	2.9	1.7	3.7	4.2	3.6472
208933_s_at	AI659005		lectin, galactoside-binding, soluble, 8 (galectin 8)	11.8	4.9	26.7	28.3	28.2	5.9	6.6	10.1	4.8	3.8	4.5	5.5	2.1	4.3	7.6	7.4	7.2	4.3	2.7	3.6311
209710_at	AL563460		GATA-binding protein 2	50.4	38.9	141.1	189.2	154.7	4.4	1.3	3.8	3.1	0.7	1.2	5.4	10.8	2.5	0.7	0.9	0.3	0.1	6.3	3.6251
205769_at	NM_003645.1		fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1)	3.3	2.5	7.0	16.2	9.2	0.3	0.3	0.3	0.5	0.1	0.4	0.2	0.3	0.2	0.4	0.7	0.1	0.3	0.1	3.5389
209409_at	D86962.1		KIAA0207	8.4	2.6	12.5	38.0	33.1	4.9	4.2	12.3	10.4	1.7	1.7	2.1	1.8	1.4	0.4	0.7	1.5	0.4	4.8	3.4907
38398_at	AB002356		KIAA0358	5.5	4.1	13.8	24.6	29.8	6.1	6.4	5.6	7.0	3.0	3.2	3.3	4.1	5.1	3.3	5.3	3.7	4.4	2.5	3.4534
205899_at	NM_003914.1		cyclin A1	5.6	3.6	16.2	20.6	10.5	0.1	0.6	0.9	0.1	1.6	0.1	0.8	0.4	1.9	0.7	0.1	0.1	0.3	0.8	3.3824
218150_at	NM_012097.1		ADP-ribosylation factor-like 5	8.2	5.3	37.6	56.6	54.6	9.1	8.6	14.0	12.1	3.9	5.0	7.7	9.6	3.8	8.3	8.1	14.5	9.9	8.1	3.3745
213097_s_at	AI338837		zuotin related factor 1	2.1	1.8	8.4	13.4	16.7	4.8	2.1	4.8	3.7	1.8	1.2	1.2	1.6	0.3	3.4	3.7	2.3	3.3	2.8	3.3672
208158_s_at	NM_018030.1		oxysterol-binding protein-related protein	1.2	2.3	8.8	18.0	15.3	0.6	0.8	1.6	1.4	1.5	2.3	2.7	1.8	2.0	0.2	0.7	1.3	0.5	4.0	3.342
210109_at	AF191492.1		nasopharyngeal carcinoma associated gene protein-8	1.2	0.7	3.6	6.4	4.2	1.2	1.6	1.0	0.3	0.6	1.1	1.7	0.6	0.2	1.3	0.5	1.4	0.6	0.1	3.2977
220918_at	NM_025143.1		FLJ20856	1.0	1.1	26.1	37.3	26.2	6.2	6.5	14.1	11.3	3.3	2.5	2.0	2.0	1.1	0.9	0.9	3.5	1.1	0.1	3.2902
209359_x_at	L34598.1		*aml 1 (acute myeloid leukemia 1) oncogene*	1.2	0.1	3.1	7.2	7.1	2.5	1.6	1.6	1.1	0.2	1.0	0.6	1.4	0.7	0.7	1.0	0.8	0.6	0.1	3.2789
208107_s_at	NM_030941.1		exonuclease NEF-sp	3.6	7.6	7.8	30.6	20.1	1.6	2.3	2.7	0.8	0.6	0.2	1.5	1.0	0.2	0.1	0.3	0.2	0.1	1.2	3.2356
212412_at	AV715767		DKFZp564A072	18.2	16.2	41.3	72.5	67.3	7.7	7.7	16.3	11.6	6.4	6.3	9.1	12.7	3.7	3.1	4.1	8.0	3.3	18.3	3.2017
215215_s_at	AC004381		chromosome 16 BAC clone CIT987SK-44M2	2.9	2.5	4.8	12.8	10.4	0.6	0.9	1.4	0.8	0.1	0.0	0.2	0.8	0.1	0.4	0.3	0.4	0.3	0.5	3.198
221509_at	AB014731.1		SMAP-3	7.6	5.4	13.2	48.5	32.4	5.2	5.7	18.1	10.7	3.5	3.8	11.4	8.1	2.8	5.6	6.0	4.1	7.5	8.0	3.1618
218637_at	NM_018439.1		hypothetical protein IMPACT	1.3	2.4	2.9	10.7	9.3	1.5	1.5	2.7	2.1	0.6	0.7	0.6	0.6	1.2	0.8	0.7	0.9	1.1	2.1	3.1587
218352_at	NM_018191.1		hypothetical protein FLJ10716	0.8	0.5	4.9	13.7	8.7	2.3	1.7	3.4	3.9	1.0	2.0	2.8	3.6	0.8	2.3	2.0	1.7	2.2	2.4	3.1058
213035_at	AI081194		KIAA0379	2.1	3.8	11.1	26.7	22.4	2.5	1.5	3.4	2.5	1.9	1.1	2.3	1.6	4.6	2.5	1.3	0.1	2.2	6.1	3.0937
211180_x_at	D89788.1		aml 1 (acute myeloid leukemia 1) oncogene	1.5	0.2	3.1	9.4	7.5	2.0	2.5	1.7	1.7	1.0	1.4	0.3	1.1	0.4	0.4	0.6	1.1	0.7	0.2	3.0936
210731_s_at	AL136105		*lectin, galactoside-binding, soluble, 8 (galectin 8)*	2.1	1.1	4.8	9.1	6.4	1.9	1.8	3.0	1.8	1.2	1.4	2.7	1.6	2.1	1.2	1.2	1.7	1.3	0.9	3.0876
203164_at	BE464756		acetyl-Coenzyme A transporter	2.3	1.9	3.7	12.6	12.4	2.5	1.9	4.0	2.7	1.1	0.6	1.2	1.7	1.4	2.3	2.6	2.1	2.7	2.5	3.063
205768_s_at	NM_003645.1		*fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1)*	3.0	1.7	3.9	10.7	7.7	0.4	0.1	0.6	0.2	0.1	0.8	0.1	0.7	0.0	0.8	0.1	0.2	0.1	0.1	3.0353
210517_s_at	AB003476.1		A kinase (PRKA) anchor protein (gravin) 12	25.1	4.9	44.0	69.5	59.6	1.5	0.4	0.6	0.8	0.1	0.2	1.0	3.0	0.9	0.8	0.5	0.1	0.3	18.8	3.0146
210647_x_at	AF102988.1		Ca2+-independent phospholipase A2 short isoform	2.3	1.1	18.7	13.2	9.1	3.4	3.3	4.0	4.5	3.3	5.0	4.2	3.6	1.8	3.5	4.4	1.8	2.8	2.2	3.002

Figure 6B

B. Eosinophil (Eo)-selective transcripts (1/1).

Probe set	Accession #		Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Eo S.I.
207328_at	NM_001140.1		15-lipoxygenase	0.1	0.6	0.7	0.1	0.1	14.5	24.6	18.3	17.0	0.1	1.1	0.1	0.1	0.1	0.0	0.1	0.0	0.1	0.0	74.129
219695_at	NM_024703.1		FLJ22593	0.0	1.0	1.8	1.8	1.1	29.8	34.7	24.8	27.8	0.8	1.5	0.4	0.9	0.1	0.6	0.4	0.3	0.1	0.1	19.123
208253_at	NM_014442.1	R	sialic acid binding Ig-like lectin, Siglec 8	1.3	2.4	0.4	0.4	0.2	17.1	23.1	17.6	11.8	0.1	0.4	0.1	0.8	0.3	0.2	0.1	0.2	0.5	0.2	9.8056
211922_s_at	AY028632.1		catalase	3.7	2.2	6.2	6.8	2.2	78.2	134.5	119.7	88.8	16.2	13.0	8.8	8.7	0.7	2.2	2.9	11.1	7.5	4.6	9.125
201802_at	NM_004955.1		solute carrier family 29 (nucleosidetransporters)	4.8	2.8	2.9	3.4	1.9	24.8	30.4	36.1	42.3	0.1	0.6	0.6	0.8	0.2	0.9	0.3	2.2	1.0	1.1	8.989
214523_at	NM_001805.1		CCAATenhancer binding protein (CEBP), epsilon	0.1	0.1	0.7	1.2	1.2	7.9	11.4	23.4	17.3	1.8	1.5	1.9	1.1	1.4	0.5	0.4	1.0	0.1	0.1	8.9462
210029_at	M34455.1		interferon-gamma-inducible indoleamine 2,3-dioxygenase	0.7	0.1	5.3	4.2	2.6	20.0	39.0	33.4	29.5	1.6	2.1	2.3	1.8	1.7	1.5	1.7	0.3	1.4	0.9	7.7078
215573_at	AU147084		FLJ12072	0.1	0.1	0.5	0.3	1.1	9.8	8.4	16.9	7.2	0.4	1.9	1.8	2.0	0.1	0.1	0.0	0.1	0.4	0.0	7.5983
201801_s_at	AF079117.1		solute carrier family 29 (nucleosidetransporters)	3.5	1.9	1.7	0.5	0.9	29.7	47.1	7.4	11.0	0.1	0.5	0.4	0.7	1.1	0.4	0.1	1.4	0.6	1.0	7.0314
213825_at	AF221520.1		oligodendrocyte lineage transcription factor 2	0.4	0.6	0.2	0.4	0.6	6.0	10.9	18.7	12.5	0.8	0.9	1.5	1.0	0.6	1.7	0.3	0.4	0.3	0.3	6.5987
219821_s_at	NM_018988.1		glucose-fructose oxidoreductase domain containing	3.0	1.4	1.8	2.6	2.3	18.7	17.3	30.9	31.3	3.9	3.1	2.4	2.9	3.2	1.3	2.5	3.0	3.8	0.8	6.2284
205472_s_at	NM_004392.1		dachshund (Drosophila) homolog	0.0	0.1	0.1	0.4	0.1	2.7	1.4	2.2	1.7	0.3	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.3	0.0	6.0088
202188_at	NM_014669.1		KIAA0095	0.5	0.9	0.4	1.8	1.2	6.8	8.5	13.5	10.6	0.2	0.2	0.2	0.1	0.2	0.3	1.7	1.7	1.4	0.4	5.4499
210548_at	U58913.1		*chemokine CCL23*	0.6	1.8	0.4	1.1	0.5	5.5	6.2	4.2	6.9	0.1	0.9	0.1	0.2	0.3	0.1	0.2	0.6	0.1	0.0	5.3082
209447_at	AF043290.1		lymphocyte membrane associated protein (8B7)	0.6	0.5	2.5	3.4	3.6	41.8	49.7	66.2	60.1	0.2	0.9	0.5	1.2	2.6	5.1	10.4	1.6	6.3	2.7	5.1472
206171_at	NM_000677.2	GPR	ADORA3 adenosine A3 receptor	2.3	2.8	2.8	3.7	2.2	7.8	13.9	22.0	17.9	1.6	3.1	2.2	2.5	1.2	1.6	0.5	2.0	0.5	0.5	5.0469
210549_s_at	U58913.1		chemokine CCL23	1.1	1.1	0.1	1.3	0.6	7.9	5.6	2.7	8.1	0.0	0.6	0.0	0.2	0.1	0.1	0.1	0.2	0.0	0.4	4.9873
214183_s_at	X91817.1		transketolase-like protein	0.1	0.2	0.2	0.1	0.1	3.2	4.0	6.6	7.2	0.2	0.2	0.1	0.1	0.2	0.2	1.0	0.1	0.6	0.0	4.7894
215350_at	AB033088.1		spectrin repeat containing, nuclear envelope 1	0.1	0.1	0.5	0.1	0.1	3.8	4.2	3.0	2.8	0.0	0.1	0.2	0.4	0.7	0.2	0.1	0.0	0.1	0.2	4.7822
206277_at	NM_002564.1	GPR	P2Y2 purinergic receptor	0.1	0.1	0.1	0.2	0.1	3.4	4.7	8.1	5.9	0.1	0.3	0.1	0.1	0.2	0.1	0.3	1.2	0.2	0.1	4.3043
204776_at	NM_003248.1		thrombospondin 4 (THBS4)	0.8	0.1	1.5	0.1	0.8	3.2	5.9	10.0	6.4	1.8	1.4	0.6	0.9	0.3	0.2	0.3	1.4	1.1	1.2	4.1746
201563_at	L29008.1		L-iditol-2 dehydrogenase	4.1	2.6	3.5	11.4	12.8	22.5	29.9	49.0	37.0	1.8	3.0	4.4	2.2	2.1	1.6	1.2	2.7	2.5	1.8	4.1557
206637_at	NM_014879.1	GPR	P2YX purinergic receptor GPR105 for UDP-glucose	5.7	1.6	13.3	19.9	13.5	44.2	55.1	81.4	62.4	1.8	9.3	15.4	9.2	0.7	0.9	0.8	0.0	5.5	0.1	3.8761
213622_at	AI733465		collagen, type IX, alpha 2	1.5	1.4	1.9	1.2	1.3	10.3	9.6	6.6	8.8	2.7	2.1	2.1	2.2	0.7	1.2	1.2	2.2	1.7	0.9	3.8576
214705_at	AJ001306.1		PDZ domain protein	0.1	0.1	0.4	0.3	0.1	2.1	1.5	2.6	2.2	0.3	0.0	0.6	0.7	0.1	0.4	0.3	0.3	0.6	0.1	3.6532
266_s_at	L33930		*CD24 signal transducer*	0.2	0.1	3.0	0.3	0.8	11.9	14.0	18.8	13.9	0.1	0.1	0.3	0.8	0.9	0.0	0.1	0.1	4.3	0.2	3.3793
201432_at	NM_001752.1		catalase (CAT)	23.0	14.3	35.7	49.4	19.9	202.3	209.7	221.6	207.3	67.0	54.3	71.3	60.9	9.2	11.2	15.1	53.6	29.9	21.4	3.3325
209696_at	D26054.1		fructose-1,6-bisphosphatase	0.9	3.4	4.3	11.1	6.4	20.2	27.7	28.8	32.5	3.0	2.5	2.4	1.6	1.9	2.0	1.6	8.1	1.1	0.6	3.3089
216379_x_at	AK000168.1		CD24 signal transducer	1.3	1.4	16.2	0.9	1.5	66.1	70.1	81.9	77.9	1.7	2.8	2.6	4.1	4.8	0.5	0.6	0.9	22.5	0.5	3.2741
205569_at	NM_014398.1		lysosome-associated membrane glycoprotein (TSC403)	0.4	0.2	0.7	0.1	0.4	2.4	3.1	6.8	3.0	0.6	0.1	1.4	0.8	0.4	1.1	0.7	0.1	0.0	0.3	3.2308
219233_s_at	NM_018530.1		hypothetical protein PRO2521	0.1	1.9	2.1	4.6	5.4	7.5	8.5	21.8	21.2	0.8	0.1	1.5	2.1	0.1	1.1	4.1	0.1	1.4	0.5	3.2093
202286_s_at	J04152		gastrointestinal tumor-associated antigen GA733-1	0.9	0.7	1.3	0.3	0.1	1.1	2.5	8.7	1.8	0.4	0.8	0.6	0.6	0.2	0.2	0.7	0.3	0.5	0.1	3.1844
206442_at	NM_003007.1		semenogelin I (SEMG1)	0.6	0.1	0.4	0.0	0.1	1.2	3.2	4.9	3.4	0.3	0.2	1.1	1.9	0.1	0.2	0.2	0.9	0.4	0.1	3.1837
205733_at	NM_000057.1		Bloom syndrome	1.9	1.1	2.0	2.4	2.2	8.5	6.0	7.5	11.2	2.1	2.0	1.0	1.2	1.2	2.4	1.8	1.1	2.6	1.2	3.1427
204392_at	NM_003656.2		calciumcalmodulin-dependent protein kinase I (CAMK1)	4.0	1.1	6.3	8.9	6.4	17.8	19.3	24.9	26.5	0.6	0.2	1.8	1.5	0.1	1.4	1.0	3.0	0.6	1.8	3.0763
213497_at	AL050374.1		DKFZp586C1619	1.0	0.7	1.0	1.3	1.6	6.3	6.8	6.8	6.0	2.3	3.0	1.4	2.3	2.0	0.4	0.5	1.6	1.1	0.8	3.0099
219296_at	NM_019028.1		similar to ankyrinrepeat-containing protein AKR1	2.2	1.7	0.2	3.5	1.6	7.3	4.4	8.4	7.4	1.8	2.4	2.4	2.3	0.1	1.4	1.6	1.3	1.9	0.8	3.0018

Figure 6C

C. Neutrophil (Ne)-selective transcripts (1/7).

Probe set	Accession #		Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne S.I.
205403_at	NM_004633.1	R	interleukin 1 R, type II	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	37.4	41.4	73.8	61.5	0.2	0.4	0.1	0.2	0.0	0.0	127.86
216782_at	AK026679.1		FLJ23026 fis	0.0	0.2	0.2	0.1	0.1	0.1	0.1	0.5	0.2	33.2	31.5	33.0	17.4	0.1	0.1	0.1	0.1	0.2	0.2	112.28
210119_at	U73191.1	ICN	KCNJ15 inward rectifier potassium channel Kir1.3	0.7	1.1	0.1	0.1	0.5	0.1	0.1	0.9	0.6	81.6	98.6	129.0	88.8	0.7	0.2	0.0	0.8	0.0	0.0	107.47
209395_at	M80927.1		*chitinase 3-like 1 (cartilage glycoprotein-39)*	1.5	0.2	0.9	0.1	0.4	0.3	0.1	8.1	0.1	28.9	25.3	70.7	40.7	0.1	0.0	0.1	0.1	0.1	0.0	79.595
203691_at	NM_002638.1		protease inhibitor 3, skin-derived (SKALP)	0.2	0.1	0.1	0.1	0.8	0.5	0.2	0.4	0.1	16.9	36.7	27.7	24.5	0.1	0.1	0.1	0.1	0.5	0.1	51.901
211372_s_at	U64094.1	R	*interleukin 1 R, type II*	0.1	0.2	0.1	0.1	0.0	0.1	0.5	0.7	0.1	21.6	36.5	31.4	29.9	0.3	0.2	0.0	0.6	0.0	0.0	50.606
207008_at	NM_001557.1	GPR	CXCR2 interleukin 8 receptor, beta	0.0	0.4	1.1	1.2	1.0	1.3	1.3	2.1	1.2	129.8	168.4	81.5	68.8	2.7	0.3	0.8	0.7	0.6	0.0	39.316
206515_at	NM_000896.1		leukotriene B4 omega hydroxylase (CYP4F3)	0.3	0.1	1.1	0.7	1.2	0.5	0.8	5.9	1.7	56.8	40.3	57.2	48.9	0.2	0.9	0.0	0.7	0.3	0.3	34.919
204007_at	J04162.1	R	Fc gamma R IIIb (CD16)	0.8	0.7	1.4	1.6	1.8	1.1	1.8	2.8	1.9	204.5	226.5	194.0	173.3	6.6	1.3	1.3	2.2	2.6	0.1	29.895
204470_at	NM_001511.1		melanoma growth stimulating activity, alpha	1.2	0.0	0.7	0.9	0.1	0.6	0.5	1.2	0.7	19.1	23.0	26.3	48.1	0.1	0.2	0.2	1.0	0.1	0.2	28.189
206025_s_at	AW188198		tumor necrosis factor, alpha-induced protein 6	0.1	0.3	0.1	0.6	0.4	0.6	0.1	0.2	0.1	19.0	29.9	17.2	24.7	0.1	0.2	0.2	0.8	0.3	0.6	26.336
209396_s_at	M80927.1		chitinase 3-like 1 (cartilage glycoprotein-39)	1.8	0.2	1.6	0.4	0.5	0.8	0.5	5.6	0.9	37.9	32.2	52.8	26.7	1.4	0.0	0.0	0.1	0.1	0.4	25.669
211806_s_at	D87291.1	*ICN*	*KCNJ15 inward rectifier potassium channel Kir1.3*	0.9	1.7	2.0	1.4	1.4	2.1	1.3	1.8	1.7	62.2	77.2	77.5	56.8	3.0	1.0	1.1	1.7	0.9	0.7	22.254
221920_s_at	BE677761		mitochondrial solute carrier	0.4	0.8	6.9	0.0	0.2	2.4	1.5	2.2	1.5	59.0	43.2	57.4	46.8	2.5	0.7	0.3	1.8	1.1	1.0	20.163
207094_at	NM_000634.1	GPR	CXCR1 interleukin 8 receptor, alpha	0.3	0.1	4.2	4.3	4.4	0.3	0.3	0.2	0.3	69.2	81.9	95.3	87.4	0.4	0.3	0.2	0.2	0.1	0.1	19.325
213589_s_at	AW468201		23614 mRNA sequence	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	5.5	2.7	5.1	4.0	0.1	0.1	0.2	0.1	0.1	0.0	18.973
218963_s_at	NM_015515.1		DKFZP434G032	0.0	0.1	0.5	0.3	0.1	1.1	2.8	2.8	2.0	46.3	32.5	40.3	31.3	0.3	0.3	0.1	0.1	0.1	0.1	18.3
213506_at	BE965369	GPR	PAR2 proteinase activated receptor-2	0.1	0.0	0.0	0.4	0.3	1.2	1.3	4.1	2.3	33.4	35.7	42.4	33.4	0.1	0.7	0.1	1.6	0.4	1.2	18.208
220187_at	NM_024636.1		FLJ23153	0.3	0.1	0.3	0.1	0.1	0.0	0.1	0.5	0.5	16.5	26.3	5.7	7.0	0.0	0.1	0.1	0.7	0.1	0.2	17.111
206026_s_at	NM_007115.1		*tumor necrosis factor, alpha-induced protein 6*	0.1	0.8	0.4	0.8	0.6	1.1	0.5	0.9	0.1	18.2	23.3	20.0	17.0	0.6	1.0	1.0	1.1	0.1	1.0	17.051
41469_at	L10343		elafin	1.2	0.7	1.2	0.8	0.8	0.9	1.0	0.7	0.8	16.2	39.1	19.5	17.4	1.3	1.4	0.7	0.8	0.5	0.5	15.913
205568_at	NM_020980.2	ICN	aquaporin 9	0.5	0.9	0.1	0.1	0.1	0.3	0.1	1.0	0.1	133.3	136.7	169.0	110.5	0.4	0.9	0.1	8.6	0.1	0.2	15.805
210483_at	BC005043.1	R	*decoy receptor 1, TRAILR3*	0.1	0.1	0.4	0.9	0.7	1.0	0.9	1.3	1.2	25.8	23.2	9.7	8.6	0.2	0.4	0.3	0.2	0.2	0.1	13.337
215223_s_at	W46388		superoxide dismutase 2	4.4	1.9	1.7	4.9	8.7	5.8	3.3	6.0	8.3	124.6	153.1	142.4	151.8	11.0	1.6	1.1	7.3	2.2	1.5	13.008
210484_s_at	BC005043.1	R	*decoy receptor 1, TRAILR3*	0.9	0.9	0.9	0.2	0.1	2.2	4.8	0.8	0.6	60.1	86.3	4.7	5.9	0.5	0.6	0.4	0.9	0.4	0.5	12.748
205654_at	NM_000715.1		complement component 4-binding protein, alpha	0.5	1.1	1.3	0.7	0.7	1.5	1.0	1.3	1.4	2.1	20.7	43.6	33.7	1.2	0.3	1.3	1.2	1.2	0.9	12.161
210773_s_at	U81501.1	GPR	formyl peptide receptor 2	0.8	0.1	0.6	0.6	0.3	0.6	0.6	0.6	0.5	86.9	105.0	50.2	59.9	0.1	1.0	0.6	6.0	0.8	0.1	12.14
206222_at	NM_003841.1	R	*decoy receptor 1, TRAILR3*	1.5	0.8	1.9	0.7	0.7	3.6	13.7	3.4	3.9	121.0	137.1	37.5	22.5	0.0	0.1	0.1	1.8	0.5	0.7	12.034
202083_s_at	NM_003003.1		*SEC14 (S. cerevisiae)-like 1*	0.8	0.2	0.9	1.8	3.0	2.2	2.6	3.8	2.6	36.7	25.9	33.9	32.6	1.3	0.1	0.1	1.1	1.0	0.7	11.729
211163_s_at	AF012536.1	R	decoy receptor 1, TRAILR3	0.2	0.1	2.2	1.5	0.6	2.6	12.3	9.4	6.4	87.9	110.9	60.4	55.8	0.5	0.2	0.1	0.7	0.1	0.6	11.404
205931_s_at	NM_004904.1		cAMP response element-binding protein CRE-BPa	0.0	0.1	0.3	0.1	0.6	0.6	0.6	0.6	0.7	23.2	14.5	20.5	12.9	1.6	0.8	0.1	1.6	0.1	0.1	10.618
205922_at	NM_004665.1		vanin 2	0.1	0.0	1.2	2.6	3.9	1.0	0.2	1.9	0.3	114.5	114.6	174.1	189.2	0.1	1.4	4.0	13.8	1.7	0.0	10.451
210176_at	AL050262.1	R	Toll-like receptor 1	0.7	0.6	0.2	0.3	0.3	0.5	1.1	1.9	1.2	29.5	38.6	25.1	32.6	1.6	0.8	0.7	3.0	1.5	0.3	10.418
215977_x_at	X68285.1		glycerol kinase	1.9	0.9	0.8	0.7	1.0	0.3	0.6	0.9	1.0	15.8	19.8	9.7	10.9	0.1	0.1	0.2	0.2	0.2	0.3	10.203
215783_s_at	X14174.1		liver-type alkaline phosphatase	0.5	1.2	0.7	0.9	0.4	0.7	0.5	1.0	0.6	21.2	42.8	11.6	12.8	1.2	0.7	0.2	0.5	0.5	1.9	10.167
217167_x_at	AJ252550		GK gene for glycerol kinase, exon 1	1.2	0.1	0.2	0.3	1.0	0.2	0.1	0.8	0.3	8.0	13.6	7.5	7.2	0.4	0.1	0.1	0.9	0.2	0.2	10.067
213349_at	AI934469		KIAA0779	0.9	0.7	0.9	1.4	1.0	1.9	1.4	2.3	2.1	15.6	15.3	19.5	23.8	0.1	1.4	1.5	1.6	1.2	1.2	9.7704

Figure 6D

C. Neutrophil (Ne)-selective transcripts (2/7).

Probe set	Accession #		Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne S.I.
210789_x_at	L00692.1		carcinoembryonic antigen (CGM1)	1.1	0.4	1.9	1.4	1.5	2.0	1.5	2.5	0.4	19.4	18.6	22.6	15.5	0.7	1.6	0.9	2.0	0.3	1.1	9.2749
210772_at	M88107.1	GPR	formyl peptide receptor 2	0.1	0.2	0.4	0.7	0.7	0.7	0.3	0.8	0.7	51.4	67.7	44.8	46.4	0.5	0.5	0.5	5.6	0.1	0.1	9.2661
218978_s_at	NM_018586.1		PRO1584	0.7	0.5	1.6	0.2	0.5	1.1	0.9	0.7	0.5	26.3	20.5	6.6	2.8	0.2	0.7	0.4	1.1	0.2	0.4	9.1536
204006_s_at	NM_000570.1	R	Fc gamma R IIIb (CD16)	0.7	0.2	1.2	0.7	0.6	0.7	0.8	0.0	0.7	230.7	278.8	47.6	45.9	4.2	1.9	6.9	12.0	3.9	0.1	9.0769
207275_s_at	NM_001995.1		fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1)	4.3	2.6	5.1	11.5	19.4	5.3	5.1	5.9	3.7	93.8	127.8	92.8	69.1	0.7	1.0	1.1	8.3	0.9	1.7	8.9855
220302_at	NM_005906.2		male germ cell-associated kinase	0.1	0.0	1.3	0.7	0.8	0.7	0.2	2.0	1.4	7.9	8.4	7.9	8.9	0.3	0.1	0.0	0.1	0.1	0.0	8.866
221803_s_at	AA883074		nuclear receptor binding factor-2	1.1	0.8	3.2	4.0	2.9	2.8	2.8	4.7	3.2	24.7	25.2	33.2	29.3	0.1	1.5	1.2	1.7	2.0	2.6	8.3788
206765_at	AF153820.1	ICN	KCNJ2 inwardly-rectifying potassium channel Kir2.1	1.0	0.4	2.5	4.4	4.4	2.4	4.7	6.1	8.0	25.8	36.2	52.4	48.3	0.4	0.2	0.5	1.5	0.7	1.1	8.108
213351_s_at	AI934469		KIAA0779	0.0	0.1	0.9	2.0	1.6	0.8	0.6	2.3	2.7	7.9	5.9	20.1	18.0	0.2	0.5	0.2	0.1	0.2	1.2	7.9705
214590_s_at	AL545760		ubiquitin-conjugating enzyme E2D 1	0.1	1.5	0.3	0.4	0.5	1.1	1.0	0.5	0.4	7.9	10.7	10.1	4.4	0.1	0.4	0.3	1.0	0.4	0.9	7.8712
206522_at	NM_004668.1		leukotriene B4 omega hydroxylase (CYP4F3)	0.0	0.0	0.8	1.8	1.0	3.0	5.4	11.7	9.4	46.0	51.5	56.9	43.0	0.1	0.0	0.0	0.6	0.6	0.1	7.5773
210992_x_at	U90939.1	R	Fc gamma receptor IIc2	1.9	1.0	1.7	2.1	3.3	8.1	16.1	2.8	4.2	70.9	95.6	42.8	30.5	0.3	0.2	0.1	7.2	2.3	0.2	7.5239
220528_at	NM_018399.1		VNN3 protein	0.1	0.2	1.3	6.1	5.0	0.2	0.1	0.5	0.4	26.8	22.1	20.0	36.8	0.8	0.2	0.1	3.0	0.1	0.1	7.5216
200919_at	NM_004427.1		early development regulator 2	5.6	4.4	4.8	6.5	9.6	7.6	6.8	5.3	7.3	109.5	89.0	52.9	61.4	2.5	4.9	7.0	10.0	3.9	6.5	7.5056
207387_s_at	NM_000167.1		glycerol kinase	2.1	1.5	1.0	1.5	1.6	1.1	1.4	1.6	1.4	14.3	20.3	10.7	10.3	0.9	0.6	0.3	1.7	0.6	0.6	7.4603
117_at	X51757		heat-shock protein HSP70B	1.1	0.2	0.8	0.6	0.9	5.9	8.3	2.1	4.1	46.3	41.2	25.1	25.8	0.4	0.9	0.6	3.7	1.6	0.5	7.4139
205174_s_at	NM_012413.2		glutaminyl-peptide cyclotransferas	0.4	0.0	0.4	0.7	0.9	0.7	0.0	0.4	0.3	30.1	47.7	36.4	24.7	0.7	0.6	0.0	4.6	0.1	1.5	7.3246
219434_at	NM_018643.1		triggering receptor expressed on myeloid cells 1	1.3	0.3	0.4	0.2	0.5	2.9	0.7	1.4	1.5	92.8	84.0	81.2	98.6	3.4	0.6	0.1	12.3	0.9	0.3	7.2368
203887_s_at	NM_000361.1		thrombomodulin	1.7	0.1	0.4	0.4	0.4	0.2	1.0	1.4	1.1	16.8	13.0	13.4	1.3	0.7	0.6	0.4	1.1	0.4	0.2	7.1328
205040_at	NM_000607.1		orosomucoid 1 (ORM1)	0.5	0.1	0.1	0.4	0.1	0.1	0.0	1.1	0.0	3.4	4.1	4.3	0.7	0.1	0.3	0.1	0.4	0.0	0.2	7.0823
214681_at	AI830490		glycerol kinase	0.2	0.4	0.1	1.2	1.7	0.8	1.1	0.6	1.2	7.8	14.2	24.0	12.1	0.9	0.0	0.1	1.9	1.0	0.3	6.966
218035_s_at	NM_019027.1		FLJ20273	2.9	1.0	0.9	1.5	0.8	0.9	0.4	1.3	1.1	47.2	54.4	91.9	94.0	1.7	0.7	0.4	9.9	1.5	0.3	6.9074
205068_s_at	BE671084		GTPase regulator associated with the focal adhesion kinase pp125(FAK)	1.2	1.4	3.5	5.9	5.1	6.5	5.1	8.5	7.1	43.7	40.6	45.2	56.0	0.7	1.3	2.9	5.1	0.8	1.2	6.8934
203021_at	NM_003064.1		secretory leukocyte protease inhibitor (antileukoproteinase) (SLPI)	1.7	0.8	4.6	1.5	1.1	1.2	2.2	8.5	0.8	16.2	19.8	13.9	8.7	1.8	0.6	1.2	1.7	1.1	2.1	6.7497
216316_x_at	X78713		glycerol kinase pseudogene, chromosome 1	2.0	0.9	0.4	0.6	1.0	0.7	0.6	0.5	1.0	10.3	18.6	5.8	5.8	0.5	0.2	0.2	0.8	0.3	0.1	6.6675
217209_at	X16454		carcinoembryonic antigen subdomains A and B	0.6	0.4	0.2	0.2	0.4	0.1	0.3	0.7	0.5	2.8	3.8	3.3	2.7	0.3	0.4	0.0	0.1	0.1	0.2	6.5382
220421_at	NM_024850.1		FLJ21458	0.3	0.6	0.1	0.1	0.1	0.3	0.8	0.4	0.3	8.9	7.2	9.1	7.0	1.2	0.6	0.0	0.1	0.1	0.2	6.4857
213524_s_at	NM_015714.1		putative lymphocyte G0G1 switch gene (G0S2)	0.8	0.8	1.3	0.9	0.5	8.0	8.5	18.7	10.1	118.0	52.0	39.6	92.5	1.7	0.8	0.1	6.0	0.2	3.4	6.4779
206472_s_at	NM_005078.1		transducin-like enhancer of split 3	2.2	2.6	1.3	0.7	0.5	1.6	0.6	0.5	1.0	22.6	25.0	11.3	8.3	1.3	1.2	1.5	1.8	1.5	0.9	6.4334
212769_at	AI567426		KIAA1547	1.4	1.5	0.5	1.3	2.3	1.1	1.0	2.2	1.9	17.9	15.9	15.1	12.8	2.4	0.8	1.1	1.3	1.2	0.5	6.4271
204307_at	AB002295.1		KIAA0329	0.7	0.0	0.1	2.6	2.1	1.8	1.5	2.4	2.0	10.3	11.2	15.4	12.8	1.9	0.1	0.5	0.2	0.1	0.5	6.3478
203591_s_at	NM_000760.1	R	granulocyte colony-stimulating factor receptor	0.1	0.0	1.0	0.1	0.2	2.3	0.6	2.4	1.0	220.3	187.2	134.9	112.1	0.2	0.8	0.2	25.5	0.1	0.2	6.2051
210210_at	AF181660.1		immunoglobulin superfamily member WM78	0.9	1.1	1.6	1.8	1.9	1.1	1.9	1.7	2.0	11.1	7.0	13.7	14.1	1.4	1.3	0.9	1.6	1.1	0.6	6.172
218610_s_at	NM_018340.1		FLJ11151	1.5	1.2	1.2	1.2	1.8	3.3	3.2	2.6	1.8	25.2	23.3	17.9	21.8	0.5	0.6	0.4	3.6	0.4	0.6	6.112
203561_at	NM_021642.1	R	Fc gamma receptor IIa (CD32)	4.7	1.2	0.9	1.2	2.4	19.5	22.8	19.4	21.4	104.3	129.0	153.0	123.9	4.0	0.7	0.7	16.3	2.2	0.2	6.1015
216841_s_at	X15132.1		superoxide dismutase 2	1.3	1.1	1.2	1.8	2.2	1.4	1.3	3.2	2.4	20.5	44.6	35.8	42.2	5.6	0.8	0.7	2.0	0.7	1.1	6.0724

Figure 6 E

C. Neutrophil (Ne)-selective transcripts (3/7).

Probe set	Accession #		Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne S.I.
207624_s_at	NM_000328.1		retinitis pigmentosa GTPase regulator (RPGR)	0.0	0.6	1.1	2.0	1.2	1.1	1.2	2.1	2.8	7.1	7.0	13.6	15.1	0.2	1.2	0.4	0.9	0.7	0.3	6.0348
209850_s_at	BC005406.1		Cdc42 effector protein 2	0.2	0.2	1.3	0.2	1.0	0.2	0.4	0.5	0.4	13.2	9.6	6.7	8.7	0.2	0.2	0.2	0.6	0.4	1.6	5.9313
203936_s_at	NM_004994.1		matrix metalloproteinase 9	47.7	0.6	1.6	1.9	1.4	1.2	2.4	15.5	1.5	36.5	35.1	36.8	21.9	1.7	2.0	1.4	1.9	1.3	1.4	5.9311
215966_x_at	AA292874		*glycerol kinase*	1.2	0.2	0.6	0.1	1.2	0.2	1.0	1.2	1.2	6.6	10.2	7.3	7.4	0.2	0.1	0.2	1.3	0.5	0.0	5.9077
206925_at	NM_005668.1		sialyltransferase 8	3.1	1.2	2.1	2.5	2.0	1.4	3.1	1.6	1.6	21.7	33.3	6.8	11.4	0.4	0.9	1.6	2.6	1.2	0.2	5.8688
211764_s_at	BC005980.1		ubiquitin-conjugating enzyme E2D 1	1.8	1.4	1.1	2.9	2.4	7.5	5.7	3.9	2.2	29.3	31.2	52.6	25.4	0.2	2.0	1.4	5.7	1.3	2.3	5.8143
201192_s_at	NM_006224.1		phosphotidylinositol transfer protein (PITPN)	3.0	3.1	1.9	5.0	4.6	3.9	5.4	6.6	5.4	27.9	26.9	32.9	35.2	2.0	3.5	3.7	5.0	3.2	2.8	5.811
205921_s_at	U16120.1		placental taurine transporter	1.2	0.7	0.5	0.2	0.4	0.3	1.6	0.5	0.9	14.8	17.2	2.8	2.6	0.0	0.1	0.3	1.1	0.3	0.4	5.7909
209137_s_at	BC000263.1		ubiquintin c-terminal hydrolase related polypeptide	3.6	4.1	2.0	2.6	1.9	1.5	0.9	2.7	0.9	25.0	24.5	37.6	29.7	3.5	5.0	2.5	3.5	2.7	3.0	5.7864
208052_x_at	NM_001815.1		carcinoembryonic antigen-related cell adhesion molecule 3 (CEACAM3)	1.7	1.4	2.9	2.7	1.9	3.0	2.6	2.8	2.1	14.3	16.5	20.0	13.7	2.5	1.3	2.3	2.8	2.5	1.6	5.7572
201393_s_at	NM_000876.1	R	insulin-like growth factor 2 receptor	6.4	2.8	0.2	0.8	1.8	4.1	5.4	6.8	5.4	82.4	106.9	80.1	71.7	1.7	2.9	8.7	8.4	4.8	14.8	5.7104
218614_at	NM_018169.1		FLJ10652	1.2	1.0	6.9	13.7	12.5	3.2	3.3	7.7	5.8	52.7	54.4	82.8	83.3	2.9	8.7	11.8	3.2	10.8	1.3	5.6442
202084_s_at	NM_003003.1		SEC14 (S. cerevisiae)-like 1	5.7	2.5	12.8	28.8	22.6	20.6	18.7	35.5	29.5	130.7	129.7	135.6	177.9	19.2	4.1	3.5	11.5	7.7	11.8	5.6423
32069_at	AB014515		*KIAA0615*	2.8	1.5	2.1	5.6	5.5	4.6	3.7	5.9	6.9	23.9	20.9	35.1	40.5	1.0	3.4	3.3	2.6	2.1	1.5	5.6348
205896_at	NM_003059.1		solute carrier family 22, member 4 (SLC22A4)	0.8	1.2	1.0	0.1	1.1	1.9	2.4	3.5	2.7	8.5	13.3	30.0	12.6	0.5	0.7	0.8	2.6	0.5	1.4	5.4612
206584_at	NM_015364.1		MD-2 protein	7.4	1.1	2.0	3.9	1.8	1.0	0.4	0.6	0.5	43.9	62.3	87.8	56.0	1.3	3.5	1.0	11.1	3.5	9.4	5.4459
202082_s_at	NM_003003.1		*SEC14 (S. cerevisiae)-like 1*	1.0	0.3	3.6	2.5	2.2	15.5	5.4	12.3	8.4	40.2	57.3	54.9	60.9	3.8	0.8	1.3	2.7	3.3	2.4	5.4422
204308_s_at	NM_014844.1		KIAA0329	2.9	1.1	2.2	2.8	2.8	2.1	3.1	3.1	4.3	16.5	18.7	19.9	19.0	3.4	1.3	1.7	1.8	1.3	2.5	5.4369
207500_at	NM_004347.1		caspase 5	0.3	1.1	0.1	0.0	0.1	0.1	0.3	0.2	0.5	4.2	6.2	4.6	2.9	0.3	0.3	0.4	0.8	0.1	0.3	5.379
203435_s_at	NM_007287.1		CD10, membrane metallo-endopeptidase	0.3	0.5	0.4	0.3	0.2	0.1	0.3	0.3	0.2	16.4	44.2	54.6	42.8	0.2	0.3	0.2	0.2	0.2	6.9	5.2591
205539_at	NM_006576.1		advillin	0.4	0.5	2.0	1.4	0.8	1.0	1.1	1.0	1.1	8.4	6.9	6.0	10.1	1.0	1.3	0.4	1.5	0.7	1.1	5.2541
204601_at	NM_014664.1		KIAA0615	1.9	1.2	1.3	3.2	2.3	3.0	2.7	3.7	3.0	12.9	12.8	20.2	20.0	0.1	2.2	2.6	1.3	1.9	1.0	5.2381
201963_at	NM_021122.2		*fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1)*	2.9	2.1	5.0	19.9	33.4	6.6	3.8	10.3	6.1	58.8	86.6	92.2	80.2	0.1	1.1	1.1	10.8	1.5	2.4	5.2374
207064_s_at	NM_009590.1	GPR	*CXCR1 interleukin 8 receptor, alpha*	0.7	0.1	0.9	0.9	0.8	0.8	0.8	0.9	1.2	4.3	4.7	4.0	6.6	0.8	0.5	0.8	0.5	0.8	0.3	5.1905
220005_at	NM_023914.1	GPR	P2YX purinergic receptor GPR86 for UDP-glucose	0.6	0.0	0.1	0.5	0.1	19.7	9.6	25.1	17.3	76.5	77.1	100.7	98.6	1.9	0.1	0.2	12.3	0.6	0.0	5.1686
211395_x_at	U90940.1	R	Fc gamma receptor IIc3	4.6	0.3	7.3	9.7	15.1	9.7	19.5	4.4	6.6	115.0	140.3	42.9	38.9	3.0	1.4	0.6	14.0	7.2	1.0	5.1401
201780_s_at	NM_007282.1		ring finger protein 13 (RNF13)	4.4	2.8	3.5	9.2	6.6	6.8	6.2	8.9	7.1	27.1	36.6	52.5	35.7	0.8	4.1	3.7	7.2	7.2	4.6	5.1305
209864_at	AB045118.1		GSK-3 binding protein FRAT2	2.8	1.3	4.4	9.2	8.0	13.4	16.9	27.3	22.6	93.2	97.2	100.6	104.2	1.3	1.9	2.9	10.2	2.5	1.0	5.1047
218319_at	NM_020651.2		pellino (Drosophila) homolog 1 (PELI1),	3.4	2.9	5.9	17.5	33.5	17.7	11.7	12.6	15.1	64.9	88.3	73.0	80.2	2.4	6.3	2.9	13.8	12.6	1.1	5.0403
206632_s_at	NM_004900.1		phorbolin	0.6	1.1	1.0	1.2	2.6	1.3	0.8	3.9	0.5	19.6	11.1	30.8	0.5	1.5	0.2	0.4	0.4	1.0	1.2	5.0277
220990_s_at	NM_030938.1		DKFZp566I133	11.7	6.2	4.6	18.5	12.5	5.0	3.3	8.2	4.9	115.5	117.2	125.3	122.5	2.6	5.3	4.2	24.1	4.4	8.3	4.9858
221653_x_at	BC004395.1		apolipoprotein L	0.7	2.8	0.6	2.1	1.6	2.0	0.4	1.8	1.1	8.0	3.9	12.7	5.2	0.2	0.9	0.4	1.4	1.1	0.4	4.9332
204748_at	NM_000963.1		COX2 prostaglandin-endoperoxide synthase 2	6.5	16.2	0.6	2.4	2.0	4.5	2.3	3.4	3.4	35.8	44.1	44.6	91.8	0.4	0.6	0.2	4.3	0.3	0.5	4.9206
210423_s_at	L32185.1		integral membrane protein	2.0	0.2	1.4	1.6	1.3	1.3	2.2	1.5	2.0	85.0	78.5	75.2	52.9	1.9	0.4	1.9	14.7	1.0	1.0	4.8845
206429_at	NM_005242.2	GPR	PAR2 proteinase activated receptor-2	0.8	0.8	0.9	0.2	0.9	0.9	1.1	0.2	0.8	11.8	15.1	4.1	4.1	1.3	1.5	0.2	1.5	0.3	0.7	4.8608
213352_at	AI934469		KIAA0779	0.6	0.9	1.2	1.5	1.2	1.2	1.5	1.5	2.2	8.4	6.0	8.7	7.7	1.6	0.9	1.5	1.0	1.3	0.8	4.8373
201888_s_at	U81379.3	R	interleukin-13 receptor	0.1	0.6	0.3	0.2	0.0	1.7	2.7	1.7	2.0	8.6	19.0	15.0	13.9	0.4	0.4	0.3	2.9	1.3	1.3	4.746

Figure 6F

C. Neutrophil (Ne)-selective transcripts (4/7).

Probe set	Accession #		Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne S.I.
204780_s_at	AA164751	R	CD95, Fas, APO-1	1.4	1.4	7.2	14.0	11.5	6.6	6.7	9.3	6.6	45.3	38.8	65.5	51.8	1.3	5.6	4.8	3.6	2.6	9.7	4.7254
209310_s_at	U25804.1		Ich-2 cysteine protease	2.5	1.9	2.1	7.7	7.0	1.4	1.3	1.3	1.4	19.1	17.5	36.7	23.5	2.9	4.1	4.5	4.9	3.9	2.2	4.6817
205452_at	NM_004855.1		phosphatidylinositol glycan, class B (PIGB)	2.3	2.7	2.3	6.4	7.7	2.3	1.4	3.0	3.0	16.3	17.6	22.2	39.3	1.7	2.0	2.9	2.8	3.5	2.2	4.6577
218298_s_at	NM_024952.1		FLJ20950	3.1	3.3	5.4	8.1	7.2	5.7	5.7	8.8	9.4	37.2	23.4	37.3	39.1	0.6	1.7	3.1	5.8	2.3	2.7	4.6558
221210_s_at	NM_030769.1		swineacylneuraminate lyase	3.8	1.2	0.8	1.2	1.4	3.0	4.7	3.2	4.6	20.4	23.6	23.5	18.3	0.6	0.1	0.3	4.6	0.5	0.1	4.6378
221497_x_at	BC005369.1		chromosome 1 open reading frame 12, clone MGC:12484	3.0	2.4	4.3	5.7	5.9	3.3	7.6	7.9	5.4	29.3	32.4	24.3	21.5	1.8	3.1	2.9	2.9	1.9	2.0	4.6333
204668_at	AL031670		ferritin, light polypeptide-like 1	0.8	0.5	1.8	1.0	1.2	0.3	1.5	1.7	0.9	8.4	8.1	7.0	6.5	1.4	1.3	1.0	1.5	0.5	1.6	4.614
201921_at	NM_004125.1		guanine nucleotide binding protein 10 (GNG10)	7.1	5.4	2.6	6.7	6.5	11.7	11.4	20.8	15.3	45.5	87.5	81.3	57.1	0.8	2.7	3.0	8.4	3.2	12.4	4.5644
209600_s_at	S69189.1		peroxisomal acyl-coenzyme A oxidase	2.9	1.7	2.8	5.3	4.7	1.4	1.0	1.2	1.3	15.0	17.7	21.4	21.2	0.4	1.0	0.8	2.1	0.7	1.5	4.5552
205119_s_at	NM_002029.1	GPR	formyl peptide receptor 1	4.1	1.4	11.2	26.6	32.7	14.0	11.1	4.2	6.0	288.2	315.8	274.7	252.9	3.6	1.3	0.7	62.6	1.1	0.5	4.505
217738_at	BF575514		*pre-B-cell colony-enhancing factor*	5.7	0.9	7.4	24.1	34.9	7.5	4.6	5.1	3.9	73.4	87.0	89.9	79.9	2.2	1.7	1.6	10.1	1.7	2.8	4.4839
215078_at	AL050388.1		DKFZp564M2422	0.0	0.1	0.0	0.1	0.4	0.9	0.5	0.8	0.3	7.1	12.9	4.5	7.9	0.1	0.5	0.5	1.7	0.1	0.1	4.4343
207545_s_at	NM_003744.1		numb (Drosophila) homolog	0.7	1.4	1.1	2.5	2.4	2.7	1.8	2.9	1.2	7.2	11.2	10.5	7.4	0.8	0.5	0.5	1.6	1.1	1.2	4.3728
213418_at	NM_002155.1		heat shock 70kD protein 6 (HSP70B)	1.1	0.4	0.7	1.5	1.6	25.3	28.8	10.5	17.0	104.0	91.6	70.0	70.8	0.5	1.1	1.1	12.8	4.7	0.5	4.3655
218023_s_at	NM_016605.1		putative nuclear protein (LOC51307)	5.7	3.8	6.6	13.0	12.6	8.5	10.3	13.0	10.9	40.1	39.7	47.0	59.7	3.0	4.4	5.9	7.0	6.0	6.8	4.3383
210386_s_at	BC001906.1		Similar to metaxin 1	6.2	1.9	2.7	5.4	4.0	1.4	2.2	1.8	3.6	19.5	15.8	23.4	23.8	2.5	3.6	2.6	4.1	2.6	4.7	4.3318
207643_s_at	NM_001065.1	R	CD120a, TNF-R-I p55	1.8	1.6	0.9	1.3	1.4	6.3	7.4	8.5	9.0	81.1	83.6	68.6	65.6	1.3	2.2	5.9	17.4	0.6	16.0	4.2796
203140_at	NM_001706.1		B-cell CLLlymphoma 6 (BCL6)	6.2	2.9	9.1	13.5	19.8	23.5	16.7	28.7	33.1	99.1	107.8	115.8	101.1	2.2	3.4	3.4	23.4	6.7	6.5	4.2767
207253_s_at	NM_016936.1		ubinuclein 1	3.2	2.8	2.9	4.4	5.0	3.8	2.6	3.8	3.6	16.7	20.0	14.2	17.8	2.3	2.5	2.5	2.2	2.4	1.8	4.2556
202875_s_at	BE397715		pre-B-cell leukemia transcription factor 2	2.0	1.4	0.1	0.1	0.2	2.5	3.6	2.1	1.5	11.6	15.4	6.8	7.5	0.8	1.7	1.9	1.1	1.3	0.7	4.2425
218791_s_at	NM_024713.1		FLJ22557	1.2	0.7	2.5	2.7	1.8	0.9	1.5	1.6	1.0	6.9	8.7	13.2	11.2	1.4	1.0	0.5	1.3	0.8	1.2	4.2114
211862_x_at	AF015451.1		Usurpin-beta	3.5	2.6	16.8	9.7	10.1	5.6	10.2	7.7	7.1	65.7	67.7	36.1	37.9	3.1	6.8	8.7	10.1	6.9	2.0	4.2001
217986_s_at	NM_013448.1		bromodomain adjacent to zinc finger domain, 1A	3.5	3.0	3.5	9.2	8.4	6.1	8.5	14.5	13.1	39.0	35.1	43.5	51.6	2.5	5.9	6.5	7.0	5.0	1.7	4.1976
217966_s_at	NM_022083.1		*niban*	4.1	1.9	6.4	7.4	9.0	24.2	14.8	25.6	11.8	51.9	105.3	76.2	80.0	0.9	3.3	3.8	3.2	2.0	8.2	4.1858
212602_at	AI806395		*KIAA0993*	2.3	3.5	0.4	0.9	1.1	0.8	0.6	0.4	0.8	17.1	18.1	12.9	13.4	1.5	0.5	0.3	3.6	0.8	2.8	4.1806
208485_x_at	NM_003879.1		CASP8 and FADD-like apoptosis regulator (CFLAR)	3.2	2.5	19.2	9.8	9.9	6.2	13.0	8.1	8.3	70.8	69.7	33.8	41.4	3.5	6.4	8.4	11.5	6.6	2.0	4.1719
201942_s_at	D85390.1		gp180-carboxypeptidase D-like enzyme	0.6	1.7	0.6	1.3	1.7	1.6	7.0	2.4	2.6	15.9	23.8	6.8	8.1	0.5	0.8	1.3	2.5	0.5	2.6	4.1525
220933_s_at	NM_024617.1		FLJ13409	2.1	2.0	9.6	14.2	14.0	7.1	7.2	10.9	12.5	38.1	37.3	81.5	57.8	1.9	3.1	4.8	6.2	3.8	3.0	4.1025
221764_at	AL574186		glycerol-3-phosphate dehydrogenase 1	6.3	4.4	16.5	18.6	15.0	10.4	15.8	21.9	22.7	80.9	99.2	46.3	60.3	9.5	8.9	9.4	5.7	9.4	2.5	4.0745
207446_at	NM_006068.1	R	Toll-like receptor 6	0.5	0.5	0.7	1.5	0.8	0.8	0.9	1.2	0.8	7.6	11.8	7.2	8.7	0.1	0.9	0.9	2.1	1.2	0.6	4.0697
219748_at	NM_024807.1		chromosome 6 open reading frame 76	0.2	0.3	0.3	0.4	0.6	1.9	2.6	1.6	1.6	9.1	9.1	6.7	6.4	0.2	0.3	0.6	0.5	1.1	0.0	4.0619
220945_x_at	NM_018050.1		FLJ10298	1.0	1.4	0.5	0.7	0.7	1.1	0.6	1.5	1.0	8.0	10.8	13.6	11.0	1.1	0.5	0.3	0.9	0.6	2.6	4.057
212577_at	AA868754		KIAA0650	1.9	1.3	6.4	8.0	9.9	10.1	24.0	8.1	9.4	74.0	98.6	42.2	57.4	4.4	10.8	9.5	7.5	16.0	3.2	4.0417
221732_at	AK026161.1		RIKEN cDNA 5830420C20	2.8	0.7	3.4	10.5	8.8	5.0	6.0	10.7	10.9	27.6	31.6	30.8	34.7	0.3	0.4	1.8	2.5	1.6	4.6	4.041
205986_at	NM_004920.1		apoptosis-associated tyrosine kinase	1.6	1.3	0.7	1.0	0.5	0.3	0.3	1.4	1.0	10.5	15.8	13.3	15.2	3.2	1.0	0.5	3.4	0.9	0.4	4.0322
213501_at	T62985		acyl-Coenzyme A oxidase 1, palmitoyl	1.3	1.1	2.0	2.6	2.8	1.3	0.9	1.2	0.6	8.5	11.5	12.4	7.5	0.1	1.1	0.3	1.8	0.5	1.1	4.0194
204542_at	NM_006456.1		sialyltransferase (STHM)	0.4	0.2	1.5	0.3	0.2	3.4	3.9	4.5	3.2	13.0	13.4	21.0	13.4	0.7	0.7	0.3	1.4	0.3	0.6	4.016

Figure 6G

C. Neutrophil (Ne)-selective transcripts (5/7).

Probe set	Accession #		Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne S.I.
204071_s_at	NM_005802.1		tumor protein p53-binding protein	1.4	1.6	1.1	3.0	2.9	3.7	2.3	2.6	2.2	10.5	12.8	8.0	11.9	1.5	2.2	2.2	1.4	2.2	2.1	4.0148
210594_x_at	AF239756.1		myelin protein zero-like 1	1.2	0.5	0.6	1.5	1.2	0.1	0.4	0.8	1.9	15.3	13.9	7.1	10.9	0.3	0.2	0.6	1.0	0.7	2.8	3.9778
203063_at	NM_014634.1		protein .phosphatase 1F (PP2C domain containing)	0.5	0.4	1.4	3.3	3.0	4.0	6.0	6.1	10.0	33.1	22.2	29.6	31.8	0.3	2.9	1.2	7.3	1.5	1.8	3.9764
201392_s_at	BG031974	R	*insulin-like growth factor 2 receptor*	1.7	0.7	0.1	0.0	0.1	2.6	3.0	1.9	1.5	51.1	59.1	12.8	15.0	1.1	1.2	4.0	3.8	2.2	7.0	3.9602
221477_s_at	BF575213		MGC:5618	2.9	1.4	3.4	4.3	9.0	4.2	4.2	4.2	4.2	56.8	63.6	36.1	46.6	7.9	3.2	1.2	12.6	2.7	2.1	3.9562
206756_at	NM_019886.1		carbohydrate (N-acetylglucosamine 6-O)sulfotransferase 7	0.2	0.1	0.1	0.0	0.1	0.1	0.1	0.1	0.1	5.0	3.9	3.5	10.5	0.1	1.3	1.0	1.0	0.2	0.5	3.9516
204994_at	NM_002463.1		myxovirus (influenza) resistance 2 (MX2)	1.3	2.3	5.4	7.8	8.2	9.2	11.6	15.2	12.3	49.8	46.6	77.6	80.8	2.4	7.5	6.0	15.6	4.8	1.8	3.9478
201943_s_at	NM_001304.2		carboxypeptidase D	0.9	0.9	0.5	2.1	3.6	1.7	7.6	7.2	4.6	16.4	21.3	18.7	15.2	0.7	1.0	1.7	3.3	0.4	3.8	3.8926
216252_x_at	Z70519.1	R	*CD95, Fas, APO-1*	0.3	0.8	4.3	2.5	1.1	1.8	4.7	1.8	1.7	18.5	31.2	10.3	8.4	2.2	3.8	2.4	1.9	1.4	3.9	3.8691
203066_at	NM_014863.1		B cell RAG associated protein (BRAG)	1.3	3.9	0.9	1.2	1.0	10.6	10.2	13.1	20.2	57.0	65.9	95.2	86.9	1.9	0.1	0.0	19.3	4.2	5.9	3.8667
212479_s_at	AL050139.1		FLJ13910	1.7	1.6	2.1	2.5	2.6	2.4	2.5	3.5	1.7	9.0	10.1	8.8	9.8	1.1	2.3	2.4	2.2	1.9	0.9	3.8422
209571_at	U03644.1		recepin	0.7	0.2	1.6	3.3	2.7	2.2	1.3	2.6	2.7	6.8	7.8	12.8	10.9	0.8	1.0	1.1	1.2	1.5	1.1	3.8367
211317_s_at	AF041461.1		*CASP8 and FADD-like apoptosis regulator*	1.6	1.8	9.5	3.6	4.0	3.7	6.8	3.2	2.8	33.1	44.8	15.2	17.6	2.4	4.7	6.5	5.7	4.9	1.1	3.8332
209732_at	BC005254.1		C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2	8.1	5.9	10.0	18.6	23.6	9.0	10.0	8.9	7.3	72.9	77.0	99.7	75.5	4.1	14.4	21.2	10.2	16.4	1.3	3.8003
201779_s_at	AF070558.1		clone 24450 RING zinc finger protein RZF	14.8	5.9	13.0	13.3	13.9	21.8	27.0	25.3	13.1	88.2	108.1	116.5	81.8	6.0	9.6	11.3	25.7	15.7	8.5	3.7993
212441_at	D86985.2		KIAA0232	5.4	2.9	3.5	9.8	10.3	8.0	6.9	11.5	11.3	31.9	30.1	30.8	49.8	2.5	2.0	4.0	5.9	2.1	4.9	3.7868
205920_at	NM_003043.1		solute carrier family 6, member 6 (SLC6A6)	1.2	1.4	0.9	0.2	0.2	1.1	5.2	0.7	1.4	33.1	26.7	2.7	4.0	0.3	0.1	0.4	2.6	0.1	0.5	3.7836
213596_at	AL050391.1		DKFZp586A181	0.7	0.7	2.3	3.6	3.0	1.2	1.2	1.1	1.2	10.6	10.9	12.5	9.9	2.2	1.1	2.0	1.5	0.7	0.3	3.7615
209508_x_at	AF005774.1		caspase-like apoptosis regulatory protein (clarp)	1.7	2.7	10.8	7.6	11.5	4.9	6.3	6.0	8.4	37.0	34.8	34.7	40.8	2.7	4.0	5.1	6.3	3.4	1.3	3.7451
218115_at	NM_018154.1		FLJ10604	0.9	2.2	2.4	1.5	0.9	1.8	2.1	1.3	1.1	10.5	9.1	6.7	7.7	1.1	1.2	2.2	2.1	1.7	1.5	3.7435
215652_at	AK024382.1		FLJ14320	0.2	0.1	2.0	0.3	1.6	0.3	0.3	1.2	0.7	5.5	4.5	3.4	2.5	0.1	0.3	1.0	0.9	0.2	0.6	3.7249
212561_at	AA349595		RAB6 interacting protein 1	10.0	6.1	10.2	12.4	11.4	18.7	14.9	12.1	10.0	66.3	60.0	47.6	37.1	4.0	8.7	9.9	13.9	5.9	10.2	3.6962
204166_at	NM_014963.1		KIAA0963	3.6	0.4	1.1	0.0	0.1	1.0	1.3	0.1	0.8	11.8	12.5	4.0	2.9	0.3	0.9	1.7	1.7	1.2	0.2	3.6908
221874_at	AB037745.1		KIAA1324	0.3	0.3	0.7	1.1	0.3	0.8	0.8	0.7	0.5	9.1	5.1	5.1	1.2	0.9	1.1	0.7	0.5	0.6	0.4	3.6808
217207_s_at	AK025267.1	R	butyrophilin like receptor	1.2	1.1	1.4	2.1	1.7	1.2	1.9	0.6	2.4	10.9	3.4	7.2	6.1	1.5	1.7	1.6	0.9	1.5	1.3	3.6795
212579_at	AA868754		*KIAA0650*	1.3	1.6	5.3	9.8	15.5	7.3	7.8	11.3	8.3	32.8	42.9	40.0	39.7	2.0	5.4	5.7	3.1	10.5	2.2	3.6784
212657_s_at	AW083357		IL-1receptor antagonist IL-1Ra (IL-1RN)	48.8	2.3	0.9	0.5	0.6	2.1	0.9	1.5	1.3	35.2	37.0	48.2	35.5	0.6	0.8	0.3	9.3	0.4	0.6	3.6759
202392_s_at	NM_014338.1		phosphatidylserine decarboxylase	3.4	2.7	6.2	11.7	6.8	3.4	4.7	5.4	4.7	32.8	31.0	22.0	32.3	0.8	1.6	1.4	4.2	1.4	1.2	3.6753
206177_s_at	NM_000045.2		arginase (ARG1)	0.5	1.3	2.2	0.4	0.6	0.9	0.8	7.2	0.7	3.9	4.3	8.1	5.0	1.1	0.1	0.4	0.6	0.7	0.0	3.6722
200706_s_at	NM_004862.1		LPS-induced TNF-alpha factor (PIG7)	31.2	39.0	20.7	64.6	62.5	15.6	13.4	31.8	21.7	173.2	148.5	172.0	150.2	8.5	13.3	42.7	14.3	16.7	18.2	3.6696
212478_at	AL050139.1		FLJ13910	0.1	0.1	0.2	2.3	3.5	1.4	0.8	1.5	1.0	3.7	3.0	4.8	6.5	0.1	0.3	1.1	0.6	0.4	0.5	3.6623
218660_at	NM_003494.1		dysferlin	2.5	0.5	1.5	0.2	0.2	1.7	0.2	2.6	1.1	48.5	51.8	44.5	20.4	3.3	1.2	1.7	10.6	0.2	1.3	3.6616
211982_x_at	AL546600		exportin 6	9.8	6.7	14.9	31.8	27.8	24.6	24.0	34.0	24.0	107.2	101.1	86.6	90.2	6.6	17.5	17.4	9.6	11.5	7.7	3.6408
202748_at	NM_004120.2		guanylate binding protein 2, interferon-inducible (GBP2)	2.4	5.3	3.7	9.0	7.4	3.3	2.1	3.0	3.3	28.1	35.2	45.0	24.8	4.2	7.3	9.0	6.3	1.9	3.7	3.6111
220088_at	NM_001736.1	GPR	C5a receptor	2.2	2.3	15.4	24.6	24.8	17.1	15.6	9.8	12.0	90.5	104.5	84.4	91.1	2.3	1.2	0.5	25.6	1.0	0.4	3.6036
202890_at	T62571		microtubule-associated protein 7	0.9	0.1	0.7	1.4	1.1	0.1	0.0	0.2	0.1	2.5	3.1	3.2	7.1	0.0	0.1	0.4	0.1	0.1	0.0	3.6032
220987_s_at	NM_030952.1		DKFZP434J037	1.4	0.3	3.9	4.9	4.7	9.6	9.3	14.1	11.7	43.0	35.6	57.8	57.6	5.3	4.7	4.8	11.1	13.3	2.0	3.5748

Figure 6H

C. Neutrophil (Ne)-selective transcripts (6/7).

Probe set	Accession #		Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne S.I.
207072_at	NM_003853.1		interleukin 18 receptor accessory protein (IL18RAP)	5.9	0.9	2.2	3.4	4.1	7.2	1.6	2.8	1.7	13.4	9.7	20.9	5.6	2.4	2.8	3.1	0.4	1.6	0.3	3.5722
215719_x_at	X83493.1	R	*CD95, Fas, APO-1*	1.0	0.6	3.1	2.7	1.6	2.2	5.2	1.8	1.7	19.0	31.9	11.4	9.4	1.0	4.5	2.2	1.6	1.1	4.4	3.5657
218404_at	NM_013322.1		sorting nexin 10	4.9	1.2	2.6	5.0	3.7	0.7	0.1	2.1	0.7	28.5	31.8	34.8	33.8	0.3	1.2	1.9	9.0	6.5	0.3	3.563
219394_at	NM_024419.1		phosphatidylglycerophosphate synthase (PGS1)	3.4	3.0	1.7	4.2	3.5	2.4	3.8	6.1	9.2	17.2	16.9	17.5	16.3	1.0	2.1	2.6	2.4	1.5	1.7	3.5544
216913_s_at	AK021460.1		KIAA0690	0.1	0.3	0.1	0.1	0.1	1.9	2.5	2.3	2.8	8.9	8.3	7.5	10.9	0.1	0.1	0.2	2.5	0.1	0.0	3.5402
205118_at	M60626.1	GPR	*formylpeptide receptor 1*	0.1	0.2	0.8	0.1	1.1	0.1	0.4	0.6	0.1	3.9	7.0	3.2	7.8	0.2	0.1	0.1	1.4	0.1	0.0	3.5295
210564_x_at	AF009619.1		*FLAME-1-delta*	1.4	1.5	5.3	6.6	7.0	4.3	4.2	5.9	3.5	21.2	30.3	18.4	19.6	2.1	2.9	4.0	4.6	3.0	1.8	3.5148
213607_x_at	BE551347		KIAA0134	1.3	1.3	2.9	2.0	1.7	8.7	15.8	3.5	4.3	42.7	42.5	11.1	15.3	0.6	1.3	1.9	6.2	1.7	0.9	3.514
203888_at	NM_000361.1		*thrombomodulin*	0.9	0.6	0.1	0.1	0.3	0.2	0.4	0.8	0.1	6.1	6.4	4.6	0.2	0.3	0.3	0.1	0.6	0.5	0.1	3.5126
210233_at	AF167343.1		interleukin-1 receptor accessory protein (IL1RAP)	0.5	0.1	0.0	0.1	0.6	0.8	0.4	0.6	0.7	1.8	3.0	2.0	2.3	0.6	0.0	0.0	0.0	0.0	0.3	3.5023
204959_at	NM_002432.1		myeloid cell nuclear differentiation antigen	1.2	0.6	24.2	50.0	26.2	17.5	17.9	49.8	22.3	249.8	290.2	186.0	217.0	3.4	1.6	0.6	66.6	2.5	0.0	3.4903
217967_s_at	AF288391.1		niban	6.3	3.7	16.3	42.4	35.9	27.9	29.5	43.0	30.9	107.4	115.3	117.9	110.3	2.6	7.5	9.9	4.9	3.4	20.4	3.4847
221763_at	AI694023		thyroid hormone receptor interactor 8	0.8	1.5	1.9	4.6	5.5	5.5	6.9	9.9	9.0	28.3	32.9	34.0	42.7	1.1	3.7	4.1	5.1	9.8	3.0	3.4777
207857_at	NM_006866.1	R	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2)	0.4	0.5	3.6	8.5	5.3	4.5	4.9	1.6	6.3	33.5	34.3	46.2	50.8	1.8	0.0	0.1	11.6	0.5	0.1	3.4773
220740_s_at	NM_005135.1		solute carrier family 12 member 6 (SLC12A6)	1.6	1.0	2.5	3.3	3.4	3.5	5.6	3.2	3.2	12.6	19.0	10.7	14.4	4.0	2.9	2.2	2.9	3.5	0.8	3.4722
217739_s_at	NM_005746.1		pre-B-cell colony-enhancing factor	7.1	1.7	9.9	46.0	61.0	18.9	13.9	12.9	9.3	112.4	120.5	90.8	93.4	1.2	2.3	1.4	17.6	2.1	3.1	3.4242
205041_s_at	NM_000607.1		*orosomucoid 1 (ORM1)*	0.3	1.0	0.4	0.1	0.1	0.0	0.1	1.0	0.1	2.6	3.6	2.7	0.4	0.1	0.2	0.1	0.5	0.0	0.1	3.4189
214784_x_at	BE966299		*exportin 6*	7.4	5.0	10.0	23.7	23.9	13.0	16.7	23.3	20.5	60.3	67.8	57.2	60.8	2.9	8.7	7.8	6.6	5.9	5.4	3.4155
217985_s_at	AA102574		*bromodomain adjacent to zinc finger domain, 1A*	1.5	1.4	1.8	2.6	3.8	7.4	5.1	7.3	4.7	16.9	19.2	22.1	24.2	2.7	2.5	2.3	3.5	2.4	0.9	3.3999
212598_at	AI806395		*KIAA0993*	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	5.5	7.3	3.1	3.2	0.2	0.1	0.0	1.0	0.1	1.3	3.3933
219053_s_at	NM_017966.1		FLJ20847	2.6	2.0	1.9	2.3	2.3	2.6	2.1	3.0	2.8	11.3	7.6	22.2	34.1	1.6	0.5	0.9	4.7	1.3	2.9	3.3686
217475_s_at	AC002073		PAC clone RP3-515N1	0.6	0.5	0.6	0.2	0.4	1.3	1.3	0.5	1.2	5.9	9.8	1.6	1.4	0.7	0.3	0.1	0.5	0.7	0.2	3.3448
46323_at	AL120741		Ca2+-dependent endoplasmic reticulum nucleoside diphosphatase	4.4	3.2	4.2	8.3	7.2	5.3	6.7	11.4	7.9	20.0	21.5	33.9	26.3	2.5	2.8	3.6	4.3	3.4	5.0	3.3028
201965_s_at	NM_015046.1		KIAA0625	2.7	3.1	3.3	8.5	8.3	4.9	5.8	7.4	7.5	19.5	18.5	18.7	27.8	2.2	3.9	3.4	4.6	5.6	2.6	3.3019
203628_at	NM_000875.2	R	insulin-like growth factor 1 receptor	0.5	0.1	3.7	3.0	4.0	6.8	4.9	2.7	5.8	18.8	23.4	6.8	20.6	1.6	0.1	2.8	2.4	2.0	3.5	3.2989
202193_at	NM_005569.2		LIM domain kinase 2 (LIMK2), transcript variant 2a	1.8	1.5	1.9	5.6	5.6	6.4	4.8	11.3	8.9	17.0	20.5	36.5	28.2	0.1	1.3	1.1	0.6	0.5	0.8	3.2887
203042_at	NM_002294.1		lysosomal-associated membrane protein 2 (LAMP2)	2.4	3.1	1.1	1.7	1.3	5.9	6.4	12.4	10.7	21.3	27.0	44.1	35.4	0.8	0.6	0.5	3.2	0.8	9.4	3.282
220326_s_at	NM_018071.1		*FLJ10357*	5.1	4.5	1.9	1.2	1.9	6.3	8.9	5.2	8.5	25.3	28.1	19.2	21.0	0.9	0.1	0.7	6.4	0.1	4.1	3.2759
212470_at	AB011088.1		*sperm associated antigen 9*	4.0	2.9	3.3	6.3	7.2	4.5	4.0	4.7	4.9	13.2	17.0	18.1	24.0	1.2	2.5	2.2	3.9	3.0	5.4	3.2688
211133_x_at	AF009643.1		*clone 6 immunoglobulin-like transcript 5*	1.9	1.4	0.8	1.5	1.3	3.1	2.7	3.8	2.1	42.1	42.2	27.0	25.1	2.7	0.9	0.5	10.2	0.4	0.2	3.2526
219313_at	NM_017577.1		*DKFZp434C0328*	0.0	0.8	0.2	0.0	0.4	0.2	0.1	0.1	0.0	3.8	3.7	3.1	5.6	0.2	0.1	0.1	0.0	1.2	0.1	3.2404
221149_at	NM_018485.1	GPR	*G protein-coupled receptor GPR77*	0.2	0.1	0.8	0.7	1.2	0.7	0.9	0.9	0.6	3.3	3.2	4.2	2.9	0.0	0.3	0.2	1.0	0.1	0.3	3.2282
203433_at	NM_006441.1		5,10-methenyltetrahydrofolate synthetase	1.4	1.8	1.5	2.5	1.6	3.1	4.2	3.5	3.1	15.8	11.4	9.6	9.0	1.6	1.8	1.9	2.9	1.7	1.5	3.2181
214486_x_at	AF041459.1		*FADD-like apoptosis regulator*	1.9	2.1	10.7	5.0	6.5	4.2	5.3	4.3	6.0	26.3	16.2	25.3	24.2	2.4	3.7	5.0	5.3	2.3	1.9	3.2114

Figure 6 I

C. Neutrophil (Ne)-selective transcripts (7/7).

Probe set	Accession #		Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne S.I.
209222_s_at	BC000296.1		oxysterol binding protein-like 2	1.3	0.2	2.7	8.8	8.0	5.4	5.4	7.7	7.3	17.2	18.4	22.3	23.9	0.9	2.3	3.4	2.8	2.0	1.3	3.1877
202334_s_at	AA877765		ubiquitin-conjugating enzyme E2B	3.3	3.4	4.8	15.5	12.1	5.3	7.2	14.7	12.8	20.9	25.6	43.6	38.1	4.0	4.5	3.9	2.5	4.9	4.6	3.1871
203266_s_at	NM_003010.1		mitogen-activated protein kinase kinase 4	3.7	2.4	4.9	8.2	6.3	2.5	4.8	6.8	5.0	14.7	15.2	27.4	26.9	2.8	2.4	2.6	2.7	2.3	2.7	3.1804
58780_s_at	R42449		FLJ10357	4.5	5.4	1.5	3.9	3.0	7.8	9.6	12.8	16.4	28.0	27.6	46.7	44.1	1.2	0.6	0.1	6.5	0.2	5.7	3.1803
210582_s_at	AL117466.1		LIM domain kinase 2	3.8	1.9	4.3	5.1	4.8	8.7	10.3	10.8	9.4	33.9	36.5	30.8	23.8	1.3	1.7	1.8	1.9	0.9	1.4	3.1609
214766_s_at	AL080144.1		ELYS transcription factor-like protein TMBS62	1.3	0.2	2.0	3.1	4.2	1.9	1.4	2.1	2.4	9.4	9.5	9.9	11.3	3.2	1.3	0.8	0.5	1.0	1.3	3.1414
202266_at	NM_016614.1		TRAF and TNF receptor-associated protein (AD022)	9.8	6.2	9.4	23.7	20.9	8.6	9.9	16.5	14.0	36.1	56.5	64.5	57.5	4.5	7.7	9.4	5.3	8.2	6.3	3.1402
203278_s_at	NM_016621.1		BRAF35/HDAC2 complex (80 kDa)	2.1	2.8	2.7	14.8	11.0	5.7	5.0	7.4	4.9	21.0	16.6	31.0	30.6	0.1	3.0	4.5	3.1	2.7	3.0	3.1382
207291_at	NM_024081.1		transmembrane gamma-carboxyglutamic acid protein 4	0.1	1.2	1.3	1.4	1.1	0.9	0.2	0.4	0.2	3.8	7.9	4.5	8.5	0.2	0.8	0.1	1.9	1.1	0.4	3.1336
213229_at	BF590131		Dicer1, Dcr-1 homolog (Drosophila)	8.5	4.5	19.5	12.9	15.4	15.9	9.7	19.1	16.0	35.2	39.0	61.4	69.4	6.2	5.9	7.3	15.2	12.2	5.0	3.1306
204204_at	NM_001860.1		solute carrier family 31	1.7	1.7	1.3	0.3	0.8	1.7	0.9	2.3	1.2	22.6	23.8	31.3	36.0	2.0	1.2	1.2	8.9	0.2	0.4	3.1262
201364_s_at	AF242521.1		ornithine decarboxylase antizyme	8.3	7.3	4.4	2.2	1.9	11.5	21.9	8.0	7.7	61.9	59.1	21.0	27.7	2.2	5.1	6.3	12.2	6.2	9.6	3.1253
210784_x_at	AF009634.1		clone 17.6 immunoglobulin-like transcript	1.4	0.1	2.1	1.2	2.4	2.5	2.2	2.8	2.1	52.1	48.8	31.8	36.3	0.8	0.2	0.2	13.3	0.3	0.2	3.1236
202625_at	AI356412		*v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN)*	6.9	6.9	5.0	18.2	14.9	20.7	21.7	27.7	28.6	74.7	76.3	77.5	75.7	7.5	1.7	0.9	17.1	23.6	0.5	3.1131
221895_at	AW469184		hypothetical protein MGC26706	2.2	0.5	5.4	5.2	5.8	5.2	3.4	7.6	5.1	14.8	12.0	24.6	19.2	2.0	2.4	2.1	5.2	1.5	1.6	3.11
37384_at	D13640		major histocompatibility complex, class I, B	2.5	3.0	3.4	3.8	3.8	6.7	6.6	7.6	6.6	25.2	17.9	21.3	29.4	2.6	2.5	2.5	7.4	1.8	2.8	3.0985
206608_s_at	NM_020366.1		retinitis pigmentosa GTPase regulator interacting protein 1 (RPGRIP1)	1.1	1.4	1.2	0.8	1.0	1.1	1.0	0.5	1.4	6.1	3.4	5.3	4.7	1.5	0.9	0.8	1.3	0.5	0.7	3.091
204924_at	NM_003264.1	R	Toll-like receptor 2	1.8	0.1	2.1	8.2	7.6	2.8	0.4	0.8	1.4	52.9	88.0	94.4	99.8	1.6	1.3	0.1	26.3	0.9	0.4	3.0909
204781_s_at	NM_000043.1	R	*CD95, Fas, APO-1*	2.0	1.1	5.9	11.0	8.9	5.4	4.4	6.8	7.0	20.6	27.1	27.0	29.1	0.3	5.2	5.3	4.0	2.0	3.8	3.0827
212606_at	AI806395		KIAA0993	2.0	2.0	0.0	0.7	0.6	0.7	0.0	0.1	0.1	18.0	14.3	25.0	26.9	0.1	0.2	0.3	6.6	0.0	3.4	3.0797
211316_x_at	AF009616.1		FLAME-1	3.1	2.9	20.1	19.4	31.9	11.6	11.9	20.6	19.1	58.8	74.1	72.8	81.0	4.1	6.8	8.7	10.3	5.5	2.6	3.0752
203045_at	NM_004148.1		ninjurin 1	4.4	2.5	3.2	6.4	4.8	10.7	9.7	18.5	12.1	29.3	34.1	44.7	46.1	0.5	1.2	1.7	8.3	0.2	2.9	3.0746
204949_at	NM_002162.2		intercellular adhesion molecule 3 (ICAM3)	3.0	3.7	5.7	46.3	34.5	38.9	51.6	94.5	93.7	161.1	168.3	239.1	241.1	4.5	13.6	21.0	17.6	19.9	1.3	3.0617
206208_at	NM_000717.2		*carbonic anhydrase IV (CA4)*	0.2	0.6	0.1	0.1	0.1	1.1	0.7	1.0	0.8	5.6	5.2	2.8	2.4	1.2	0.1	0.1	0.1	0.1	0.1	3.0572
213727_x_at	AI743654		metallo phosphoesterase	2.1	1.7	5.0	15.0	12.1	8.9	13.7	25.4	23.9	49.9	28.3	59.9	75.8	0.7	4.5	6.6	5.7	5.4	3.7	3.0554
202626_s_at	NM_002350.1		v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN)	15.5	9.5	12.1	12.7	14.8	32.6	31.6	54.0	41.0	110.1	115.1	122.7	127.2	18.4	2.1	1.5	36.8	33.0	0.6	3.0541
206420_at	NM_005849.1		immunoglobulin superfamily, member 6 (IGSF6)	1.1	0.3	0.2	0.4	0.7	1.9	1.2	1.1	1.0	17.5	24.2	30.6	33.3	1.4	0.4	0.4	8.4	0.3	0.3	3.0442
201651_s_at	NM_007229.1		protein kinase C and casein kinase substrate in neurons 2 (PACSIN2)	21.4	17.4	4.6	24.8	20.1	13.3	19.5	33.9	35.3	61.3	72.5	76.1	94.4	24.7	4.9	4.4	8.6	6.1	8.0	3.0391
219540_at	AU150728		zinc finger protein 267	2.0	1.0	1.3	3.7	3.6	2.0	1.5	4.4	3.7	6.7	6.9	9.2	9.9	1.0	2.1	1.3	1.0	1.6	0.1	3.0361
201244_s_at	NM_002880.1		v-raf-1murine leukemia viral oncogene homolog 1 (RAF1)	6.0	5.4	12.4	32.8	33.1	14.9	19.0	27.3	25.7	60.4	58.2	89.2	86.2	2.2	6.6	11.3	12.8	7.6	7.3	3.0329
203265_s_at	AA810268		mitogen-activated protein kinase kinase 4	1.4	1.2	2.8	6.4	4.5	1.7	2.6	3.5	3.1	12.8	12.8	10.4	16.8	1.4	1.4	1.3	1.3	2.5	1.5	3.028
203030_s_at	AF007555.1		IAR receptor-like protein-tyrosine phosphatase	0.0	0.0	1.6	1.2	0.1	0.1	0.1	0.1	0.1	0.8	3.0	1.1	2.8	0.1	0.1	0.0	0.1	0.0	0.0	3.0269
203739_at	NM_006526.1		zinc finger protein 217	1.9	2.6	3.0	18.4	8.4	7.6	8.0	14.7	14.9	37.3	45.1	24.4	27.0	1.2	4.6	5.3	6.1	5.5	3.6	3.0158
204747_at	NM_001549.1		interferon-induced protein with tetratricopeptide repeats 4 (IFIT4)	2.0	3.0	4.9	6.0	3.5	4.3	12.4	4.4	3.0	24.2	27.0	15.4	12.0	0.3	1.8	1.2	6.2	1.4	2.6	3.0143
206209_s_at	NM_000717.2		carbonic anhydrase IV (CA4)	0.7	1.0	0.8	0.6	0.6	2.2	2.1	1.5	2.1	13.8	7.4	4.7	3.5	2.1	1.0	0.5	0.9	1.0	0.5	3.0112

Figure 6J

D. Mast cell (MC)-selective transcripts (1/2).

Probe set	Accession #		Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	MC S.I.
217023_x_at	AF099143		*tryptase beta*	**169.4**	**118.7**	*0.7*	1.1	*0.4*	*0.1*	*0.1*	*0.5*	*0.1*	*0.2*	*0.1*	*0.6*	*0.4*	*0.3*	*0.1*	*0.1*	*0.2*	*0.1*	*0.2*	202.148
215382_x_at	AF206666.1		*tryptase beta*	**168.1**	**108.4**	**1.7**	*0.7*	*0.4*	*0.2*	*0.2*	*0.2*	*0.1*	*0.1*	*0.3*	*0.1*	*0.1*	*0.7*	*0.1*	*0.1*	*0.1*	*0.1*	*0.5*	172.668
204041_at	NM_000898.1		monoamine oxidase B	**23.5**	**46.9**	*0.2*	*0.7*	*0.1*	*0.1*	*0.2*	*0.6*	*0.3*	*0.3*	*0.1*	*0.2*	*0.1*	*0.2*	*0.2*	*0.1*	*0.2*	*0.1*	*0.2*	136.311
210084_x_at	AF206665.1		*tryptase alpha*	**131.1**	**92.3**	*0.7*	*1.2*	*1.2*	*0.2*	*0.1*	*0.1*	*0.1*	*0.1*	*0.1*	*0.1*	*0.1*	*0.6*	*0.1*	*0.0*	*0.1*	*0.1*	*0.1*	112.376
216474_x_at	AF206667.1		tryptase beta	**210.0**	**120.9**	*2.4*	2.0	*1.4*	*1.2*	*0.4*	*0.2*	*0.1*	*0.2*	*1.1*	*0.1*	*0.1*	*1.8*	*0.8*	*0.9*	*0.9*	*0.1*	*0.1*	84.3375
205683_x_at	NM_003294.2		*tryptase beta*	**195.5**	**95.3**	*2.4*	*2.7*	*0.3*	*0.2*	*0.2*	*0.6*	*0.6*	*0.4*	*0.1*	*0.4*	*1.0*	*2.0*	*0.7*	*0.2*	*0.3*	*0.2*	*0.1*	67.2617
207741_x_at	NM_003293.2		tryptase alpha	**175.0**	**99.7**	*2.2*	*2.2*	*1.8*	*0.5*	*0.2*	*0.3*	*0.2*	*0.6*	*0.2*	*0.3*	*0.3*	*2.2*	*0.7*	*0.1*	*0.5*	*0.3*	*0.6*	59.015
207134_x_at	NM_024164.2		*tryptase beta*	**214.6**	**112.3**	*3.1*	**3.8**	*1.7*	*1.2*	*0.3*	*0.8*	*0.6*	*0.3*	*0.8*	*0.4*	*0.1*	*0.5*	*0.2*	*0.1*	*1.1*	*0.4*	*0.2*	57.1834
205653_at	NM_001911.1		cathepsin G	**91.2**	**57.0**	*2.7*	*1.1*	**0.9**	*0.9*	*0.4*	**3.1**	*0.8*	*0.3*	*1.4*	*1.6*	*0.6*	*0.7*	*0.2*	*0.4*	*1.3*	*0.3*	*0.2*	51.4749
205266_at	NM_002309.2		leukemia inhibitory factor	**17.0**	**9.8**	*0.2*	*0.2*	*0.3*	*0.3*	*0.1*	*0.2*	*0.2*	*0.1*	*0.2*	*0.4*	*0.7*	*0.1*	*0.2*	*0.1*	*0.1*	*0.1*	*0.1*	44.3659
210324_at	M17263.1		complement protein C8 gamma	**2.9**	**6.9**	*0.1*	*0.1*	*0.0*	*0.0*	*0.0*	*0.1*	*0.1*	*0.3*	*0.1*	*0.1*	*0.1*	*0.1*	*0.1*	*0.0*	*0.0*	*0.0*	*0.1*	33.806
211743_s_at	BC005929.1		major basic protein	**74.3**	**70.7**	*1.0*	**4.7**	**2.7**	*0.1*	*0.7*	*0.8*	*0.6*	*0.2*	*0.3*	*0.7*	*0.2*	*0.1*	*0.2*	*0.2*	*0.3*	*0.2*	*0.3*	31.5959
211549_s_at	U63296.1		*15-hydroxyprostaglandin dehydrogenase*	**48.3**	**48.3**	**2.1**	**2.5**	*1.4*	1.5	**1.3**	*0.8*	*0.9*	*0.1*	*0.1*	*0.2*	*0.1*	*1.1*	*0.5*	*0.8*	*0.5*	*0.5*	*0.0*	24.8454
206726_at	NM_014485.1		prostaglandin D2 synthase	**119.0**	**94.0**	**5.0**	**7.8**	**5.7**	*0.7*	*0.1*	*1.0*	*0.5*	*0.2*	*0.2*	*0.2*	*0.6*	*1.3*	*0.7*	*0.3*	*1.2*	*0.3*	*0.0*	17.432
205011_at	NM_014622.1		loss of heterozygosity, 11, chromosomal region 2, gene A	**76.1**	**70.9**	**3.0**	**6.8**	**4.5**	*2.3*	*1.0*	*1.4*	*1.9*	*0.2*	*1.1*	*1.2*	*1.8*	*2.9*	**2.2**	**1.3**	**1.7**	**2.0**	**2.6**	16.2511
205428_s_at	NM_001740.2		calbindin 2	**16.7**	**63.4**	*1.3*	**0.7**	0.9	*0.4*	*1.6*	*0.7*	1.3	*1.8*	*1.6*	*3.6*	*1.5*	*1.7*	*0.7*	*1.1*	*1.3*	*0.6*	**0.9**	16.1621
219225_at	NM_024554.1		FLJ11413	**10.0**	**9.2**	*0.1*	*0.1*	*0.1*	*0.2*	*0.1*	*0.6*	*0.6*	*0.1*	*0.6*	*0.1*	*0.2*	*0.1*	*0.6*	*0.1*	*0.6*	*0.0*	*0.2*	15.639
204468_s_at	NM_005424.1		tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	**3.6**	**2.8**	*0.5*	*0.3*	*0.1*	*0.0*	*0.1*	*0.2*	*0.0*	*0.0*	*0.0*	*0.1*	*0.1*	*0.0*	*0.0*	*0.0*	*0.1*	*0.0*	*0.0*	14.4259
208343_s_at	AF146343.1		CYP7A promoter binding factor	**1.5**	**0.9**	*0.0*	*0.0*	*0.3*	*0.1*	*0.0*	*0.1*	*0.0*	*0.1*	*0.0*	*0.2*	*0.4*	*0.1*	*0.0*	*0.0*	*0.0*	*0.0*	*0.0*	13.8025
205051_s_at	NM_000222.1	R	CD117 c-KIT	**92.1**	**85.8**	**6.2**	**8.1**	**7.3**	**2.3**	**5.2**	**6.5**	**2.7**	*0.7*	*2.1*	*0.8*	*1.1*	*0.8*	*0.2*	*0.5*	*0.1*	*0.1*	*0.5*	12.3815
210102_at	BC001234.1		*loss of heterozygosity, 11, chromosomal region 2, gene A*	**40.9**	**41.1**	**2.8**	**3.7**	**4.5**	*0.3*	*0.4*	*0.3*	*0.6*	*0.7*	*0.9*	*0.2*	*0.6*	**1.8**	**0.8**	*0.7*	**1.2**	*0.6*	**1.3**	11.3619
210796_x_at	D86359.1		*sialic acid binding Ig-like lectin, siglec6*	**17.8**	**26.0**	*1.5*	**1.0**	*1.1*	**1.2**	1.5	1.3	*1.4*	*1.4*	**2.3**	*1.7*	1.3	*2.0*	*1.4*	1.5	*1.8*	**1.0**	**0.8**	10.5398
206519_x_at	D86358.1	R	sialic acid binding Ig-like lectin, siglec6	**3.4**	**7.9**	*0.0*	*0.3*	*0.4*	*0.0*	*0.0*	*0.0*	*0.1*	*0.0*	*0.1*	*0.5*	*0.2*	*0.5*	*0.0*	*0.0*	*0.0*	*0.4*	*0.0*	10.13
206480_at	NM_000897.1		leukotriene C4 synthase	**8.8**	**16.0**	*0.3*	*0.2*	*0.6*	**2.4**	**1.6**	**0.5**	*0.1*	*0.2*	*1.1*	*0.1*	*0.1*	*1.3*	*0.1*	*0.3*	*0.1*	*0.1*	*0.4*	9.27381
206617_s_at	NM_002910.4		renin-binding protein	**10.6**	**6.2**	*1.2*	*0.1*	*0.4*	**2.8**	*1.6*	*0.5*	*0.1*	*0.6*	*2.1*	*0.1*	*0.1*	*0.9*	*0.2*	*0.7*	*0.3*	*0.4*	*0.1*	9.18529
208089_s_at	NM_030794.1		tudor domain containing 3	**6.0**	**13.4**	*0.8*	*0.6*	*0.2*	**0.5**	0.7	**0.5**	*0.5*	*0.1*	*0.6*	*0.3*	*0.0*	*0.7*	**0.7**	**1.1**	*0.8*	**0.6**	**1.0**	8.16897
205466_s_at	NM_005114.1		heparan sulfate 3-O-sulfotransferase	**18.1**	**7.2**	*0.1*	*0.4*	*0.1*	*0.7*	*0.1*	*0.3*	*0.2*	*0.4*	*0.1*	*0.8*	*0.4*	*0.1*	*0.0*	*0.0*	*0.2*	**1.4**	*0.0*	8.15381
214913_at	AB002364.1		ADAMTS3 a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3	**6.8**	**4.3**	*0.5*	**0.7**	**0.8**	*0.5*	*0.7*	*0.6*	*0.4*	*0.5*	*0.4*	**0.7**	**1.2**	*0.7*	*0.6*	**0.5**	*0.4*	*0.5*	**0.5**	7.2214
201860_s_at	NM_000930.1		tissue-plasminogen activator	**22.2**	**29.7**	*0.2*	*0.4*	*0.1*	*0.1*	*0.3*	*0.5*	*0.5*	*0.1*	*0.1*	*1.3*	*0.4*	*1.6*	*0.1*	*0.2*	*0.6*	*0.1*	**3.6**	7.10135
206520_x_at	NM_001245.1		*sialic acid binding Ig-like lectin, siglec6*	**19.0**	**22.7**	*2.4*	*1.1*	*0.8*	*1.1*	*1.5*	1.3	*1.0*	*2.0*	*2.0*	*0.4*	*1.4*	*2.9*	*2.1*	*2.3*	*1.9*	*1.9*	*1.2*	7.10132
220532_s_at	NM_014020.1		LR8 protein	**52.4**	**18.2**	*0.8*	*0.8*	*1.0*	**6.4**	**2.9**	*1.5*	*1.2*	*0.4*	*0.3*	**1.4**	*0.6*	*2.2*	*0.6*	*0.2*	**5.0**	*0.1*	*0.0*	6.1662
218169_at	NM_018052.1		FLJ10305	**6.2**	**14.6**	*0.3*	*0.2*	*0.4*	*0.4*	*0.3*	*0.3*	*0.4*	*0.6*	*0.5*	*0.1*	*0.1*	*0.5*	*0.2*	*1.4*	*1.6*	*0.3*	*1.0*	6.04597
221728_x_at	AK025198.1		nuclear receptor subfamily 1, group I, member 3	**5.6**	**5.5**	*0.6*	*0.9*	*1.0*	*0.4*	**3.6**	*0.9*	*0.8*	*0.7*	*0.6*	*1.4*	*0.9*	*0.9*	*0.8*	*0.7*	*0.7*	*0.8*	*0.5*	5.70228
214028_x_at	AU156998		*tudor domain containing 3*	**3.2**	**11.9**	*0.9*	*0.0*	*0.4*	*0.8*	*0.3*	*0.4*	*0.7*	*0.6*	*0.6*	*0.1*	*0.1*	*0.8*	*1.2*	**1.1**	*0.1*	**0.7**	*0.9*	5.10738
221552_at	BC001698.1		lipase	**10.6**	**3.4**	*0.9*	*1.8*	*1.1*	*0.9*	*1.1*	*1.0*	*0.9*	*0.2*	*0.2*	*0.7*	*0.1*	*0.1*	*0.2*	*0.7*	*0.9*	*0.3*	*1.1*	5.02434
203367_at	NM_007026.1		MKP-1 like protein tyrosine phosphatase (MKP-L)	**15.0**	**45.4**	*1.2*	*0.9*	*0.8*	*0.9*	*0.9*	*0.8*	*0.1*	*0.2*	*0.7*	*0.4*	*2.0*	*0.9*	**1.0**	**2.7**	*0.5*	**1.4**	**5.2**	5.00514
206997_s_at	NM_004807.1		heparan sulfate 6-O-sulfotransferase	**4.2**	**3.8**	*0.2*	*0.1*	*0.1*	*0.4*	*0.4*	*0.1*	*0.3*	*0.3*	*0.4*	*0.3*	*0.7*	*0.3*	**0.2**	**0.6**	*0.3*	**0.8**	**0.2**	4.81127

Figure 6K

D. Mast cell (MC)-selective transcripts (2/2).

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	MC S.I.
207480_s_at	NM_020149.1	TALE homeobox protein Meis2e	14.0	14.9	1.9	3.6	4.0	1.7	1.9	5.3	3.8	0.3	0.6	1.0	0.3	0.5	0.8	0.4	0.6	0.4	0.8	4.72642
45288_at	AA209239	*lipase*	10.9	3.0	0.2	2.1	0.8	0.5	0.5	1.3	0.9	0.1	0.1	0.2	0.1	0.4	0.5	0.5	1.3	1.0	0.9	4.52869
207039_at	NM_000077.1	*cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)*	7.5	3.6	0.7	0.7	0.1	0.6	0.4	0.3	0.5	0.1	1.2	0.6	1.1	0.1	0.9	0.5	0.8	0.1	1.2	4.35629
201650_at	NM_002276.1	keratin 19	6.2	12.0	0.0	0.0	0.3	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.1	0.1	0.0	0.1	0.1	0.0	2.0	4.35547
214533_at	NM_001836.1	chymase	10.1	2.7	0.4	0.2	0.8	0.1	0.1	0.8	0.6	0.1	0.1	0.2	0.2	1.2	0.7	0.5	1.0	0.4	0.3	4.27984
218211_s_at	NM_024101.1	melanophilin	24.8	29.6	2.7	2.5	1.8	3.0	2.5	1.9	2.2	4.6	4.1	3.3	4.1	6.4	4.0	3.2	2.4	3.4	2.7	4.24499
203916_at	NM_003635.1	N-deacetylaseN-sulfotransferase	17.9	26.7	3.2	6.5	6.8	2.5	2.7	3.6	3.1	4.2	3.4	5.5	5.2	0.9	3.1	4.9	3.3	2.7	2.4	4.20693
212336_at	AB002336.1	erythrocyte membrane protein band 4.1-like 1	3.8	6.4	0.1	0.2	0.1	0.5	0.1	0.2	0.4	0.1	0.1	0.1	0.5	0.1	0.4	0.2	0.4	0.4	1.2	4.12758
200766_at	NM_001909.1	cathepsin D	42.6	39.5	2.5	5.3	4.3	4.3	4.8	3.4	2.7	4.0	6.7	3.1	1.9	2.6	1.6	2.5	10.0	1.6	5.9	4.1037
202218_s_at	NM_004265.1	delta-6 fatty acid desaturase (FADSD6)	18.8	24.5	0.4	0.2	1.0	0.3	0.1	0.8	0.5	0.2	0.1	0.1	0.1	1.6	0.1	0.6	0.1	0.6	5.3	4.08548
204066_s_at	NM_014914.1	centaurin, gamma 2	5.3	7.9	0.4	0.4	0.7	0.2	0.2	0.6	0.6	0.3	0.5	0.4	0.4	0.8	0.6	1.6	0.6	1.0	1.6	4.06712
209644_x_at	U38945.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	14.0	6.4	1.0	1.4	0.7	1.2	1.3	1.7	1.5	1.0	1.6	1.5	2.1	2.3	1.8	1.5	0.9	0.3	2.4	3.88459
221679_s_at	AF225418.1	*lipase*	2.8	1.9	0.4	0.9	0.1	0.3	0.4	0.4	0.1	0.1	0.5	0.0	0.5	0.5	0.1	0.6	0.6	0.5	0.2	3.83039
211538_s_at	U56725.1	heat shock protein 70kD	4.4	7.4	0.3	0.6	0.4	0.6	0.3	0.3	0.9	1.4	0.4	1.0	0.8	1.5	0.5	0.5	0.1	0.5	0.7	3.80423
211548_s_at	J05594.1	*15-hydroxyprostaglandin dehydrogenase*	82.6	60.0	19.4	26.0	16.3	3.2	2.9	1.8	1.7	0.8	0.5	0.9	0.2	4.1	1.2	0.9	0.1	0.6	0.2	3.49258
210174_at	AF228413.1	nuclear receptor subfamily 5, group A, member 2	2.9	3.4	0.5	0.5	0.6	0.8	1.1	0.7	1.2	1.1	0.4	0.1	0.4	0.9	0.7	0.2	0.2	0.6	0.3	3.47124
219412_at	NM_022337.1	RAB38, member RAS oncogene	3.9	4.0	0.1	0.4	0.3	0.7	0.1	0.2	0.3	0.2	0.2	1.1	0.1	1.2	0.1	0.8	0.4	0.1	0.5	3.32805
201850_at	NM_001747.1	gelsolin-like capping protein (actin filament)	70.5	64.5	9.6	30.8	28.8	8.1	7.8	11.5	9.9	2.6	3.6	3.0	2.4	1.6	1.1	1.0	17.0	5.8	5.3	3.29919
205888_s_at	AI962693	KIAA0555	5.4	4.6	0.7	1.6	1.2	0.8	0.7	0.1	1.0	1.3	0.3	0.2	0.6	1.2	0.3	1.5	0.7	1.2	0.4	3.25197
221750_at	BG035985	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	5.0	3.8	0.9	1.5	1.1	1.1	1.2	1.3	1.0	1.3	0.5	0.7	1.2	0.7	0.5	1.1	0.7	1.4	1.2	3.1926
214218_s_at	AV699347	*nuclear receptor subfamily 1, group I, member 3*	3.5	3.5	0.7	0.6	0.7	0.5	2.2	0.5	0.5	0.7	1.2	0.6	0.1	1.1	0.9	0.3	0.6	0.8	0.4	3.15254
218788_s_at	NM_022743.1	FLJ21080	16.1	23.7	0.5	2.3	2.5	0.9	1.1	2.7	2.1	1.1	1.0	0.8	0.9	2.3	2.1	2.9	0.6	2.0	6.3	3.07851
218087_s_at	NM_015385.1	SH3-domain protein 5 (ponsin)	1.4	1.9	0.4	0.9	0.4	0.5	0.0	0.0	0.1	0.0	0.1	0.1	0.2	0.1	0.0	0.2	0.2	0.2	0.1	3.07366
221577_x_at	AF003934.1	prostate differentiation factor	7.8	5.5	0.6	0.3	0.5	0.6	0.1	0.2	0.6	0.0	0.2	0.3	0.1	0.1	0.2	0.0	0.1	0.4	2.1	3.05532
35820_at	X62078	GM2 activator protein	21.8	17.6	1.4	3.3	1.3	0.3	0.3	0.2	0.5	0.5	0.8	1.9	0.3	0.4	0.2	0.2	6.5	5.0	2.7	3.01647
208744_x_at	BG403660	heat shock 105kD	7.3	4.8	0.5	0.2	0.2	0.9	0.1	0.4	0.6	0.1	0.1	0.3	0.1	0.8	1.7	2.0	0.9	0.9	2.0	3.00671

Figure 6 L

E. Basophil and eosinophil-selective transcripts (1/1).

Probe set	Accession #		Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba+Eo S.I.
211517_s_at	M96651.1		*IL-5R interleukin 5 receptor alpha*	0.6	0.1	11.8	28.2	17.9	16.4	25.3	32.6	29.5	0.0	0.7	0.0	1.0	0.0	0.4	0.2	0.0	0.2	0.0	61.956
210744_s_at	M75914.1	R	IL-5R interleukin 5 receptor alpha	0.2	1.6	15.4	30.8	15.3	18.7	40.2	29.7	33.0	0.3	0.2	1.5	0.5	0.1	0.1	0.1	0.1	0.2	0.1	42.811
206361_at	NM_004778.1	GPR	CRTH2 chemoattractant receptor-homologous molecule expressed on Th2 cells	1.8	0.3	22.0	40.5	15.3	33.7	37.9	38.9	42.3	1.0	2.6	2.2	2.1	0.8	1.4	1.0	1.2	0.9	0.5	16.642
206207_at	NM_001828.3		Charcot-Leyden crystal protein	1.1	0.1	270.0	219.1	203.6	226.8	233.8	179.7	163.1	2.1	19.4	19.1	49.3	2.8	1.0	1.4	0.9	0.7	0.4	15.164
203638_s_at	NM_022969.1	R	fibroblast growth factor R 2	0.2	0.1	7.3	43.5	33.0	4.1	8.8	12.3	23.3	0.1	0.1	0.3	0.3	0.1	0.1	0.2	0.1	0.1	1.0	13.357
207111_at	NM_001974.1	GPR	egf-like module containing, mucin-like, hormone receptor-like sequence 1 (EMR-1)	1.5	0.1	16.4	49.5	34.5	85.9	93.1	91.2	93.5	2.7	3.7	5.4	5.1	3.4	1.7	0.8	7.1	1.6	0.5	8.0092
215248_at	AU145003		FLJ11581 fis, clone HEMBA1003598	0.7	0.3	5.7	4.7	5.2	4.5	2.1	2.8	2.1	1.0	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.2	7.2618
205471_s_at	AW772082		dachshund (Drosophila) homolog Hs.63931	0.1	0.6	5.1	4.1	3.7	6.4	8.3	9.0	7.6	0.8	0.9	1.0	0.8	0.1	0.1	0.3	0.5	0.0	0.1	6.8198
218857_s_at	NM_025080.1		FLJ22316	1.0	7.0	18.0	35.3	18.6	13.7	12.5	16.3	15.4	1.3	1.7	0.9	1.9	0.3	0.5	0.4	2.4	0.2	0.2	6.5045
221169_s_at	NM_021624.1		*histamine receptor H4*	0.2	0.5	4.5	12.5	8.9	1.9	2.6	4.2	2.9	0.5	0.6	1.1	0.6	0.4	0.7	0.5	0.7	0.0	0.3	5.9783
201769_at	NM_014666.1		enthoprotin	7.8	9.1	41.7	101.5	76.0	26.8	34.1	40.5	35.7	3.0	2.9	3.6	4.2	4.5	6.3	6.9	8.0	9.0	7.9	5.1015
208228_s_at	M87771.1		secreted fibroblast growth factor receptor (K-sam-III)	0.3	1.4	3.7	10.2	8.3	3.9	8.9	4.5	8.3	0.8	1.4	1.1	0.5	1.3	0.4	0.7	0.3	0.5	1.1	4.9922
213605_s_at	AL049987.1		hypothetical protein, MNCb-4779	0.8	0.0	10.8	46.8	44.7	6.7	6.1	25.8	20.6	1.3	1.4	4.5	4.2	2.9	1.1	2.1	3.7	2.0	0.3	4.7426
205382_s_at	NM_001928.1		adipsin	3.5	0.1	62.0	206.0	176.5	62.4	48.1	60.5	44.8	7.1	32.5	20.5	16.3	0.1	0.6	0.1	15.6	0.1	3.8	4.7202
49452_at	AI057637		*hypothetical protein LOC283445*	0.6	0.2	5.2	7.7	6.6	6.9	5.9	10.2	12.7	1.1	0.2	0.3	1.3	0.1	1.6	1.6	0.5	1.3	0.8	4.7183
220307_at	NM_016382.1	R	CD244 natural killer cell receptor 2B4	0.5	0.1	15.7	87.0	65.4	9.9	10.8	26.6	18.5	0.3	0.4	1.2	3.0	0.1	0.4	3.5	5.2	1.1	0.1	4.6297
210108_at	BE550599	ICN	calcium channel, voltage-dependent, L type, alpha 1D subunit	0.2	0.1	1.0	1.7	2.4	0.9	0.8	2.4	1.8	0.0	0.6	0.5	0.5	0.0	0.3	0.1	0.0	0.3	0.0	4.5958
209193_at	M24779.1		protein kinase-related oncogene (PIM1)	6.8	7.1	61.3	110.3	100.1	47.0	79.7	91.6	79.5	19.2	18.8	21.1	16.1	4.1	12.7	13.9	4.6	4.0	1.2	4.1983
202794_at	NM_002194.2		inositol polyphosphate-1-phosphatase (INPP1)	5.7	6.2	7.1	25.8	20.5	17.9	24.8	53.6	57.8	2.8	2.7	2.6	4.0	1.9	1.8	2.6	4.8	1.9	4.8	4.1158
208304_at	NM_001837.1	GPR	CCR3 chemokine (C-C motif) receptor 3	0.2	1.1	107.2	142.9	102.2	46.4	91.7	118.1	107.5	28.3	20.0	26.3	25.1	0.2	0.5	0.4	0.2	0.2	0.4	3.9525
206111_at	NM_002934.1		eosinophil-derived neurotoxin	2.2	2.0	33.7	71.4	38.4	104.7	80.8	47.7	45.1	2.0	2.3	3.1	2.8	1.4	0.7	0.4	14.8	0.7	0.5	3.7641
43427_at	AI970898		hypothetical protein LOC283445	0.8	0.7	2.1	4.8	4.3	5.1	4.6	8.0	6.4	1.0	0.8	0.7	0.8	1.1	1.0	1.3	0.6	1.1	1.1	3.7554
213804_at	AI039084		inositol polyphosphate-5-phosphatase, 75kD	0.6	1.2	4.3	8.0	6.8	8.6	5.6	6.3	9.7	0.7	0.5	2.2	1.7	1.4	1.2	1.4	1.0	1.9	1.3	3.6088
209906_at	U62027.1	GPR	C3a receptor	12.4	11.2	44.1	72.3	50.5	18.8	38.8	70.3	29.9	1.2	1.2	1.8	3.8	1.6	1.6	1.5	3.0	0.6	0.5	3.6039
202804_at	AI539710		ATP-binding cassette, sub-family C (CFTRMRP), member 1	8.5	7.0	24.2	56.2	48.9	14.2	20.0	30.1	20.7	3.0	3.6	4.3	6.0	3.8	3.5	5.4	5.1	5.5	5.3	3.5673
221675_s_at	AF195624.1		cholinephosphotransferase 1 beta	7.0	6.8	31.6	79.7	55.8	26.9	32.6	43.8	41.8	5.2	7.5	5.9	9.6	2.4	3.1	3.3	7.7	11.8	5.7	3.5626
201562_s_at	NM_003104.1		sorbitol dehydrogenase (SORD)	2.0	1.5	2.9	4.2	4.1	7.4	11.6	8.3	11.2	1.7	2.5	1.5	1.3	1.3	1.4	1.8	1.2	1.8	1.1	3.5098
210230_at	BC003629.1		FLJ23438 fis, clone HRC13275	1.1	0.1	8.3	11.0	13.3	2.4	5.1	5.1	4.1	0.1	0.5	0.2	0.7	0.3	0.2	0.6	0.8	1.9	0.5	3.2532
219919_s_at	NM_018276.1		FLJ10928	0.1	0.2	3.1	1.8	2.5	1.7	4.3	1.7	2.1	0.1	0.5	0.4	0.3	0.1	0.1	0.1	0.1	0.1	0.7	3.2497
204301_at	NM_014867.1		KIAA0711	0.6	0.1	3.8	14.3	10.7	5.3	6.8	12.6	10.5	1.2	0.6	1.6	1.6	1.0	0.8	1.2	2.6	0.8	0.1	3.2398
210999_s_at	U66065.1		Grb10- and Grb-IR-related splice variant 1	3.6	1.7	8.4	13.6	11.8	7.3	4.6	4.8	6.4	2.2	1.7	1.9	2.0	1.9	1.2	1.2	1.6	0.4	1.6	3.1044
209539_at	D25304.1		RacCdc42 guanine exchange factor (GEF) 6	13.1	24.8	28.8	74.7	73.0	53.8	35.5	92.9	59.6	9.2	6.1	18.5	13.7	3.1	10.8	12.9	7.1	7.8	1.0	3.0943
208921_s_at	L12387.1		sorcin (SRI)	19.2	11.4	20.2	88.6	67.0	37.4	42.4	86.3	85.4	6.9	8.9	17.6	21.5	2.6	11.1	12.7	8.4	8.6	17.8	3.0628
209043_at	AF033026.1		bifunctional ATP sulfurylaseadenosine 5-phosphosulfate kinase	19.9	16.1	39.0	87.1	75.2	66.4	68.7	89.4	71.4	13.8	20.0	46.5	8.9	6.3	6.7	4.4	10.6	11.0	22.7	3.0385

Figure 6M

F. Eosinophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #		Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Eo+Ne S.I.
221345_at	NM_005306.1	GPR	GPR43, PAR1-like	0.1	0.4	0.9	0.6	0.6	7.0	16.6	15.4	10.5	49.7	45.7	22.5	23.0	0.8	0.1	0.1	0.7	0.4	0.1	21.742
212860_at	BG168720		zinc finger, DHHC domain containing 18	2.2	0.8	4.1	3.9	4.0	16.0	17.4	14.8	16.7	59.2	53.9	30.9	39.8	1.1	2.4	3.8	2.6	1.5	1.3	6.5842
211576_s_at	BC003068.1		solute carrier family 19 member 1	1.4	0.1	0.7	1.4	0.7	5.1	5.9	11.5	12.4	19.8	18.7	27.1	28.1	1.8	0.9	0.4	2.7	0.5	0.8	4.99
214321_at	BF440025		nephroblastoma overexpressed gene	1.3	1.0	0.8	0.2	0.7	6.2	7.2	17.0	13.7	4.5	7.6	10.7	11.3	0.1	0.1	0.0	0.1	0.1	1.8	4.9823
218950_at	NM_022481.1		ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3	1.4	3.1	2.4	3.7	2.1	15.5	15.9	18.3	15.5	28.0	24.3	15.9	20.6	0.7	0.2	0.8	3.9	0.9	1.0	4.829
205681_at	NM_004049.1		BCL2-related protein A1	0.5	1.9	1.0	3.2	2.4	52.4	40.2	35.9	30.5	46.5	49.2	35.5	33.5	1.5	2.2	1.9	8.3	4.3	0.2	4.7782
203765_at	NM_012198.1		grancalcin	2.0	1.8	4.5	11.7	8.3	27.5	39.8	46.7	34.8	71.6	85.2	80.5	77.9	1.0	1.0	1.2	12.1	3.1	0.5	4.4403
213241_at	AF035307.1		cDNA FLJ36416 fis, clone THYMU2011053	5.0	2.4	1.6	1.0	1.0	33.2	37.1	68.7	40.6	63.2	77.8	89.2	80.9	3.0	3.0	2.8	13.5	4.1	7.8	4.2603
221815_at	BE671816		hypothetical protein PRO2831	1.2	1.4	1.3	0.5	1.6	10.1	8.8	11.2	6.4	5.0	6.2	4.0	3.8	1.6	0.8	0.2	1.4	0.9	0.6	4.1325
214153_at	BE467941		homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2	1.0	0.6	1.0	2.0	3.1	9.1	10.4	18.2	16.6	9.7	9.7	14.5	15.2	0.8	0.9	1.2	0.7	2.3	0.1	4.0797
212821_at	AU147160		KIAA0599	0.1	0.1	0.4	1.2	0.9	4.6	2.8	4.7	3.4	4.4	3.5	6.0	7.9	0.4	0.2	0.4	0.3	0.0	0.2	3.727
206723_s_at	AF011466.1	GPR	Edg4, endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4	1.2	1.4	2.1	3.6	2.6	13.7	8.0	19.6	22.3	24.6	17.0	26.1	29.1	0.1	3.6	5.0	3.8	1.9	0.9	3.7119
212360_at	AI916249		adenosine monophosphate deaminase 2 (isoform L)	1.0	2.0	2.6	5.9	4.6	26.6	18.7	30.2	31.9	78.7	63.1	79.5	91.3	3.4	5.8	6.1	12.6	3.7	5.8	3.5888
218308_at	NM_006342.1		transforming, acidic coiled-coil containing protein 3 (TACC3)	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	0.7	3.4769
212629_s_at	AK023692.1		protein kinase C-like 2	1.9	0.6	3.1	3.7	5.1	11.8	7.6	17.7	13.8	16.7	23.6	27.0	28.4	1.1	2.1	2.2	4.2	4.2	2.9	3.2963
201739_at	NM_005627.1		serumglucocorticoid regulated kinase (SGK)	30.2	25.2	1.9	18.5	25.4	114.1	116.0	150.9	164.8	60.2	77.1	105.8	156.3	1.1	3.7	0.7	34.6	1.6	18.9	3.2456
209473_at	AV717590		ectonucleoside triphosphate diphosphohydrolase 1	1.4	0.8	2.1	1.6	2.0	15.9	22.3	39.5	29.1	14.1	13.7	23.7	13.8	2.6	2.6	1.3	6.5	4.8	0.6	3.0752
209304_x_at	AF087853.1		growth arrest and DNA damage inducible protein beta (GADD45B)	2.0	0.3	2.7	4.5	3.6	15.5	11.9	16.3	34.4	7.0	12.0	13.5	9.4	0.4	3.1	4.2	4.1	3.7	0.6	3.0295
210666_at	AF050145.1		iduronate 2-sulfatase	0.1	0.3	1.3	0.5	1.7	7.1	2.9	3.3	3.8	6.1	5.1	5.2	10.8	0.4	0.1	0.9	0.7	0.4	0.1	3.0005

Figure 6 N

G. Basophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba+Ne S.I.
218739_at	NM_016006.1	CGI-58 protein	1.8	1.8	7.2	16.3	17.3	2.6	3.3	3.2	2.5	20.7	23.6	21.4	19.3	1.3	1.2	0.7	2.9	0.7	1.5	5.81398
219242_at	NM_025180.1	FLJ13386	1.0	0.3	10.1	23.5	18.8	2.4	3.7	4.5	4.2	13.7	14.0	26.1	27.7	0.1	0.5	1.6	1.0	0.6	2.5	4.97025
219157_at	NM_007246.1	kelch (Drosophila)-like 2	2.4	1.7	4.2	16.2	19.2	3.6	2.5	4.3	3.8	15.5	24.4	24.5	22.5	0.7	2.0	1.5	3.0	2.2	1.7	4.61523
206643_at	NM_002108.2	histidine ammonia-lyase	0.1	1.4	8.5	13.7	25.4	0.2	0.6	1.3	0.6	31.4	32.8	61.7	37.0	1.6	0.5	0.1	5.6	0.6	0.5	4.57355
213935_at	AF007132.1	clone 23551 mRNA	0.8	0.1	5.0	26.2	26.4	2.4	1.7	2.9	1.2	4.5	6.7	11.2	9.0	0.1	0.1	0.2	2.3	0.5	0.8	4.33664
222151_s_at	AK023738.1	FLJ13676 fis	1.0	0.9	4.5	5.5	4.7	1.8	1.7	1.4	1.6	8.4	10.2	8.4	7.6	0.5	0.8	1.3	0.8	1.0	1.3	4.14372
207907_at	NM_003807.1	tumor necrosis factor (ligand) superfamily, member 14 (TNFSF14)	0.1	0.1	3.9	10.4	6.3	1.2	1.5	4.0	4.1	15.8	7.3	15.8	11.5	0.2	0.4	0.1	0.6	0.0	0.1	3.89177
202530_at	NM_001315.1	mitogen-activated protein kinase 14	5.0	3.0	28.8	82.2	70.8	4.0	7.1	13.9	11.1	13.6	23.0	25.7	22.3	5.3	2.9	3.5	7.3	2.6	4.5	3.8469
217521_at	N54942	Hs.276590 ESTs	0.1	0.1	5.5	18.9	20.9	0.3	0.3	1.6	0.1	19.6	14.5	29.9	18.4	0.4	0.8	0.9	4.3	1.0	0.3	3.84207
203693_s_at	NM_001949.2	E2F transcription factor 3	2.5	1.7	4.3	16.2	13.2	2.1	1.9	5.7	3.3	8.8	11.7	13.3	15.4	1.5	1.4	2.5	2.3	1.1	1.2	3.7116
203420_at	NM_016255.1	autosomal highly conserved protein (AHCP)	2.4	3.3	15.6	31.5	32.4	7.3	6.6	14.3	11.0	37.2	37.2	48.5	50.0	6.1	5.0	9.8	4.5	3.3	9.8	3.48188
218308_at	NM_006342.1	transforming, acidic coiled-coil containing protein 3	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	0.7	3.4769
203080_s_at	NM_013450.1	bromodomain adjacent to zinc finger domain, 2B	2.2	2.4	10.4	22.8	22.9	4.9	6.6	10.0	9.5	29.5	30.7	33.5	40.6	1.1	1.7	1.9	4.6	2.3	1.5	3.401
219999_at	NM_018621.1	hypothetical protein PRO2198	0.4	0.6	3.9	7.6	8.0	2.0	1.5	3.9	2.7	9.8	6.5	11.7	12.3	0.2	1.3	1.8	2.4	1.7	0.9	3.31991
213805_at	AI692428	clone 23551 mRNA	0.3	0.1	13.8	11.0	8.7	3.2	3.0	1.4	1.4	19.7	16.7	5.3	7.0	0.7	0.2	0.8	3.3	0.4	0.7	3.29317
204669_s_at	NM_007219.2	ring finger protein 24	0.9	0.2	4.4	27.9	34.3	2.1	5.9	16.1	14.5	18.8	14.4	60.7	56.1	0.5	0.1	0.1	0.1	0.1	0.8	3.18834
215555_at	AK023774.1	FLJ13712 fis	0.0	0.4	5.0	4.3	5.8	1.5	1.9	1.5	1.5	7.6	8.2	3.3	3.2	0.9	1.0	1.5	1.5	1.0	0.1	3.1591

Figure 60

H. Mast cell and basophil-selective transcripts (1/1).

Probe set	Accession #		Transcripts	MC. cord blood	MC. lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb	MC+Ba S.I.
205624_at	NM_001870.1		carboxypeptidase A3	137.1	91.0	107.6	139.0	173.1	2.5	1.6	2.8	1.9	0.1	1.4	2.0	12.4	0.2	1.2	0.2	0.2	0.5	0.5	59.1989
208605_s_at	NM_002529.2	R	TRK neurotrophin receptor	8.0	1.2	4.6	9.3	8.1	0.2	0.2	0.0	0.1	0.2	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	34.7309
210258_at	AF030107.1		regulator of G protein signaling (RGS13)	6.2	8.4	5.6	7.1	10.9	0.3	0.1	0.4	0.5	0.5	0.0	0.1	0.3	0.1	0.0	0.0	0.2	0.3	0.0	21.7762
207496_at	NM_000139.1	R	Fc epsilon R I beta	19.9	24.7	35.4	51.9	45.6	0.9	0.1	0.5	0.3	0.1	0.1	0.5	1.8	1.6	0.5	0.2	0.0	0.3	0.1	21.1783
205857_at	AI269290		solute carrier family 18	24.3	27.1	8.1	22.3	25.0	1.3	1.0	0.8	0.9	1.3	0.9	0.5	0.7	0.9	0.4	0.3	0.2	0.3	0.3	20.3301
210358_x_at	BC002557.1		GATA-binding protein 2	18.4	12.8	55.0	31.7	24.7	2.0	1.6	1.9	1.7	0.9	1.9	1.3	3.7	2.6	0.8	0.8	0.9	0.4	2.7	9.46893
207497_s_at	D10583.1		*Fc epsilon R I beta*	10.7	28.6	34.9	12.6	6.8	1.5	1.0	0.8	0.8	1.9	0.9	1.7	1.5	1.7	0.7	0.7	0.1	0.3	0.5	9.39967
203914_x_at	NM_000860.1		*15-hydroxyprostaglandin dehydrogenase (PDGH)*	63.9	51.4	24.8	36.0	23.3	4.1	4.6	4.6	2.6	1.3	0.9	1.3	1.2	6.0	1.4	1.5	0.4	0.8	0.4	6.14285
219557_s_at	NM_020645.1		chromosome 11 open reading frame 14	7.4	4.2	4.4	7.4	6.6	1.2	1.6	2.0	2.4	0.9	1.9	1.1	2.1	1.1	1.4	1.4	1.5	0.4	1.6	3.38029
204061_at	NM_005044.1		protein kinase, X-linked	6.2	5.2	5.2	12.8	16.9	2.3	2.7	2.5	2.4	0.8	0.4	0.7	1.2	1.9	1.5	2.1	2.5	2.0	0.8	3.26062
202068_s_at	NM_000527.2	R	low density lipoprotein receptor	24.6	16.8	19.3	28.5	13.5	1.6	1.0	1.6	0.9	0.8	2.4	1.5	2.5	2.3	2.1	3.4	3.5	0.8	6.3	3.1679

Figure 6P

I. Specific transcripts markers for non-granulocytes.

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb
203547_at	U47924	CD4	**5.5**	**4.7**	*2.2*	*1.1*	*1.2*	*2.0*	*1.6*	*0.4*	*0.9*	*0.7*	*1.1*	*0.7*	*0.8*	*3.5*	**15.0**	*0.3*	**17.6**	*1.2*	*0.4*
205758_at	AW006735	CD8	*0.5*	*1.7*	*2.6*	*2.3*	**3.2**	*1.3*	*1.1*	*2.2*	*1.7*	*0.3*	*0.5*	*1.8*	*0.3*	*4.2*	*3.0*	**76.1**	*0.8*	*0.6*	*0.4*
206398_s_at	NM_001770.1	CD19	*0.7*	*0.1*	*0.7*	*0.4*	*0.7*	*0.8*	*0.5*	*0.5*	*0.2*	*0.6*	*1.5*	*1.1*	*0.7*	**4.0**	*0.0*	*0.1*	*0.1*	**19.1**	*0.4*
211644_x_at	L14458.1	IgG V-J region	*0.2*	*0.1*	*0.1*	*0.1*	*0.2*	*0.2*	*0.2*	*0.2*	*0.3*	*0.1*	*0.3*	*0.2*	*0.2*	*3.8*	*0.1*	*0.2*	*0.1*	**70.9**	*0.1*
201743_at	NM_000591.1	CD14	**18.4**	*2.4*	*0.3*	*0.1*	*0.6*	**8.8**	*0.6*	*1.1*	**3.2**	**40.7**	**49.6**	**58.7**	**68.2**	*2.9*	*0.4*	*0.0*	**97.2**	*1.1*	*0.9*
203104_at	NM_005211.1	v-fms M-CSF receptor	**3.8**	*0.2*	*0.6*	*0.7*	*0.3*	**3.0**	*1.1*	*1.7*	*1.5*	**8.8**	**8.7**	**6.3**	**6.4**	*5.2*	**2.8**	*0.7*	**42.1**	*1.4*	*0.9*
209968_s_at	U63041.1	CD56	*0.1*	*0.1*	*0.1*	*0.1*	*0.1*	*0.1*	*0.1*	*0.2*	*0.1*	*0.1*	*0.1*	*0.2*	*0.1*	*0.1*	*0.1*	*0.1*	*0.2*	*0.1*	*0.0*
204627_s_at	M35999.1	CD61 glycoprotein IIIa	**1.7**	**9.4**	*0.2*	*0.1*	*0.3*	*0.1*	*0.1*	*0.1*	*0.1*	*0.1*	*0.4*	*0.1*	*0.2*	**48.3**	*0.1*	*0.3*	*0.1*	*0.2*	*0.5*
216442_x_at	AK026737.1	fibronectin	*0.3*	*1.5*	*0.3*	*0.3*	*0.2*	*0.1*	*1.0*	*0.3*	*0.6*	*0.1*	*0.1*	*0.2*	*0.1*	*0.3*	*0.1*	*1.0*	*0.3*	*0.1*	**92.6**

Figure 6 Q

J. Raw AD levels for the median values used to normalize the raw AD levels, and the housekeeping genes.

Probe set	Accession #	Transcripts	MC, cord blood	MC, lung	Ba 1	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD4	CD8	CD14	CD19	Fb
AFFX-HSAC07/X00351_3_at	X00351	beta-actin	18534	19383	14638	20922	19151	22019	18638	21153	18568	19406	22302	16589	17569	18295	18782	20805	20661	17542	20399
AFFX-HSAC07/X00351_M_at	X00351	beta-actin	22898	21777	12940	11533	7608	22560	18785	14861	13431	23106	23373	6861	8019	19368	20362	22761	22294	19087	22757
AFFX-HSAC07/X00351_5_at	X00351	beta-actin	15642	15838	9516	2927	2066	17186	21061	4861	3771	18772	19768	2165	2193	14887	16381	18218	17583	15063	16795
AFFX-HUMGAPDH/M33197_3_at	M33197	GAPDH	14906	13632	3640	10477	9332	2649	2844	5498	2605	2549	3186	3586	3538	5929	6429	6098	9756	5180	19674
AFFX-HUMGAPDH/M33197_M_at	M33197	GAPDH	15891	16852	3218	7587	6963	2382	2565	3720	1838	2194	2796	2312	2154	6182	5931	5921	11464	4344	17013
AFFX-HUMGAPDH/M33197_5_at	M33197	GAPDH	16298	16701	3479	4559	5110	1827	3121	2127	1168	2492	3476	1636	1355	4655	6826	6260	9905	5636	23350
The median value of 22283 transcripts			121	169.3	85.3	112.2	110.9	93.7	102.1	127.3	114	62.7	73.1	87.4	87.3	82.3	152.5	121.3	107.1	114.1	183.8

Abbreviations used in the table A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

Figure 6 R